



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 123519**

**TO: Christopher Yaen**  
**Location: REM/3A20/3C18**  
**Art Unit: 1642**  
**June 4, 2004**

**Case Serial Number: 09/700770**

**From: P. Sheppard**  
**Location: Remsen Building**  
**Phone: (571) 272-2529**

**sheppard@uspto.gov**

### **Search Notes**

STIC-Biotech/ChemLib

193519

From: Yaen, Christopher  
Sent: Wednesday, June 02, 2004 10:33 AM  
To: STIC-Biotech/ChemLib  
Subject: 09700770

could you please search seq id 7, 8, and 9

thanks

Chris

Christopher Yaen  
US Patent Office  
Art Unit 1642  
571-272-0838  
REM 3A20  
REM 3C18

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 20:07:29 ; Search time 16.6872 Seconds  
(without alignments)  
1966.411 Million cell updates/sec

Title: US-09-700-770-9

Perfect score: 502

Sequence: 1 MKLALLGLCVALSAAAA.....QAVGAVKALKALGALTVEG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacterioph.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225	44.8	94	11 Q8CJC6	Q8CJC6 mus musculus
2	88	17.5	255	16 Q82LN6	Q82LN6 streptomyc
3	83.5	16.6	281	16 Q8FST3	Q8FST3 streptobacte
4	82.5	16.4	247	16 Q9K3G4	Q9K3G4 streptomyc
5	82.5	16.4	694	16 Q98CRL	Q98CRL rhizobium l
6	81	16.1	496	10 Q9SU83	Q9SU83 arabidopsis
7	80	15.9	148	16 Q9XW23	Q9XW23 raietonia s
8	79	15.7	136	16 Q82R50	Q82R50 streptomyc
9	77.5	15.4	229	16 Q7WJ56	Q7WJ56 bordetella
10	77.5	15.4	229	16 Q7WA34	Q7WA34 bordetella
11	77.5	15.4	229	16 Q7VYAI	Q7VYAI bordetella
12	77.5	15.4	601	16 Q86691	Q86691 streptomyc
13	77	15.3	453	17 Q8THL0	Q8THL0 methanosarc
14	76	15.1	355	16 Q8UAI4	Q8UAI4 agrobacteri
15	76	15.1	699	16 Q9ABL0	Q9ABL0 caulobacter
16	76	15.1	889	16 Q8G4X4	Q8G4X4 bifidobacte

17 75.5 15.0 459 16 Q9E2L6 streptomyc  
18 75.5 15.0 496 16 Q8G3S5 bifidobacte  
19 75.5 15.0 544 17 Q9YEG2 aeropyrum p  
20 75.5 15.0 667 16 Q8XRM8 raietonia s  
21 75 14.9 299 16 Q89XU3 streptomyc  
22 75 14.9 355 2 Q8RPK5 corynebacte  
23 75 14.9 370 16 Q89H46 bradyrhizob  
24 75 14.9 463 11 Q8C3I3 mus musculu  
25 74 14.7 611 16 Q9L0K1 streptomyc  
26 73.5 14.6 119 5 Q86DI1 leishmania  
27 73.5 14.6 331 17 Q9HN19 halobacteri  
28 73.5 14.6 358 16 Q8NQ28 corynebacte  
29 73.5 14.6 389 16 Q8EJ01 streptomyc  
30 73.5 14.6 1468 5 Q9GUB5 shewanella  
31 73 14.5 317 16 Q8D48 rhizobium l  
32 73 14.5 429 16 Q825M1 streptomyc  
33 73 14.5 502 16 Q9I5I2 pseudomonas  
34 73 14.5 542 10 Q8GYA1 arabidopsis  
35 73 14.5 584 16 Q9AAR5 caulobacter  
36 73 14.5 620 16 Q7WL37 bordetella  
37 73 14.5 620 16 Q7W7Q0 bordetella  
38 73 14.5 1279 5 Q46099 drosophila  
39 73 14.4 240 2 Q84CV5 gamma-prote  
40 72.5 14.4 373 5 Q7WYC1 toxoplasma  
41 72.5 14.4 384 16 Q88KE1 pseudomonas  
42 72.5 14.4 421 2 Q93I77 thermus the  
43 72.5 14.4 482 5 Q9BHF9 leishmania  
44 72.5 14.4 616 16 Q7W2M5 bordetella  
45 72.5 14.4

## ALIGNMENTS

RESULT 1

Q8CJC6 PRELIMINARY; PRT; 94 AA.  
AC Q8CJC6; DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE UGRF2 type B.  
GS SCGB3A1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22326074; PubMed=12438750;  
RA Nini T., Copeland N.G., Gilbert D.J., Jenkins N.A., Srisodhai A.,  
Zimonjic D.B., Keck-Waggoner C.L., Popescu N.C., Kimura S.;  
RT "Cloning, expression, and chromosomal localization of the mouse gene  
RT (Sc33a1, alias Ugrp2) that encodes a member of the novel uteroglobin-  
RT related protein gene family.";  
RL Cytogenet. Genome Res. 97:120-127(2002).  
DR EMBL; AF313457; AAN62328.1; --  
DR MGD; MGI:1915912; Scgb3a1.  
SQ SEQUENCE 94 AA; 9578 MW; 7C84B908A6365B59 CRC64;

Query Match

Best Local Similarity 44.8%; Score 225; DB 11; Length 94;

Matches 51; Conservative 14; Mismatches 20; Indels 4; Gaps 2;

QY 17 SAAPFLVGSAPVQAPVAALSAEAAAGAGTIAN-PLGTINPLKLLLSGLGIPVNHLEGS 75

9 SVAFEMDSLAKPAVEPVAAALAAEAVAGVPSPLSHLAIIRFLILASGMGIPLDLEGS 68

QY 76 QKCAEVLGPQAVGAVKALKALGALTVEG 104

69 RKCVELGPEAVGAV---KSLGLVLTWFG 94

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RESULT 2
Q82LN6 PRELIMINARY; PRT; 255 AA.
AC Q82LN6;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Putative methionine aminopeptidase.
GN SAV1374.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=1262562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:528-531(2003).
DR EMBL; AP005029; BAC69685.1; -
DR GO; GO:0004239; F:methionyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000994; Peptidase M24.
DR InterPro; IPR002467; Pept M24_MAP1.
DR InterPro; IPR001714; Pept M24_MAP.
DR Pfam; PF00557; Peptidase M24; 1.
DR PRINTS; TIGR00500; met pdase I; 1.
DR TRIFAMS; TIGR00500; met pdase I; 1.
KW Aminopeptidase; Complete proteome.
SQ SEQUENCE 255 AA; 26727 MW; 0C41CD3010F955A3 CRC64;

Query Match 17.5%; Score 88; DB 16; Length 255;
Best Local Similarity 31.6%; Pred. No. 2.7;
Matches 31; Conservative 16; Mismatches 19; Indels 32; Gaps 6;

QY 7 LGLCVA---LSCSSAAFLVGSAPVAPVVALE-----SAAEAGA--GTLANPL 51
DB 99 LDLAVARGVADRAISFLVGKARP-AESVAMTERALAAAGIAKFGARIGDLSHAI 157

QY 52 GTLNPLKLLSSLGIPVNHLEIGSKVCVABLGPOAVGA 89
DB 158 GT-----VLSKAGVPIN-----TEFGHGIGS 179

RESULT 3
Q8FST3 PRELIMINARY; PRT; 281 AA.
AC Q8FST3;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN CE0299.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RN [2]
SEQUENCE FROM N.A.

RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005215; BAC17109.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 281 AA; 2818 MW; 3143B69C35048C2D CRC64;

Query Match 16.6%; Score 83.5; DB 16; Length 281;
Best Local Similarity 30.1%; Pred. No. 7.7;
Matches 40; Conservative 9; Mismatches 45; Indels 39; Gaps 7;

QY 3 LAALIGLCV-----ALSCSSAAFLVGSAPVAPVVALESAAE-----AGAGTL 47
DB 106 LAGFLGICIGNLRAGAPMADAMDHAAHTTGTSGSAGPTTVALTAARRVRSGGGAANL 165

QY 48 ANP-----LGTLL-----NPLKLLSSLGIPVNHLEIGS-----QKCVABLGPOAV 87
DB 166 IDAPTMOLQRLGTVWEVSERHGIFLVRLDQL-----KRLAQERHQASAAQLQGPAT 221

QY 88 GAVKALKALIGAL 100
DB 222 AVILALLPLAGVL 234

RESULT 4
Q9K3G4 PRELIMINARY; PRT; 247 AA.
AC Q9K3G4;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein SC01277.
GN SC01277 OR 2SCG18.24.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939108; CAB99157.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 247 AA; 22950 MW; EE32ABD76146881B CRC64;

Query Match 16.4%; Score 82.5; DB 16; Length 247;
Best Local Similarity 31.8%; Pred. No. 8.3;
Matches 34; Conservative 10; Mismatches 40; Indels 23; Gaps 5;

QY 17 SAAAFVGSAPK-----VAOPVAALESAAEAG-----AGTLANPLGTL-----NPLKL 59
DB 61 NALAALAGAVNPATALAGVTNPALAGGIGAGNPLAGLAGAAGPLGNTAGAAQNPLAA 120

QY 60 LLSSL--GIPVNHLEIGSKVCVABLGPOAVGAKKALLKALGVFG 104
DB 121 LTGAGGNGNPLAALGGAGNPLAALG-----GAANPLAAGVGAAGALG 163

RN [1]
RN [2]
SEQUENCE FROM N.A.

```



DE Putative membrane protein.  
GN BFL449.  
OS Bordetella pertussis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Acaligenaceae; Bordetella.  
CX NCBI\_TaxID=520;  
RN [1]  
RP SEQUENCE FROM N.A.  
SP STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;  
RX MEDLINE=22827954; PubMed=12910271;  
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,  
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
RA Cordero-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,  
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,  
RA Leather S., Mounie S., Norberczak H., O'Neill S., Ormond D., Price C.,

Thu Jun 3 10:25:06 2004

us-09-700-770-9.rspt

Page 3

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RESULT 5
Q98CRI
ID Q98CRI PRELIMINARY; PRT; 694 AA.
AC AC
DT DT
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein mlr5043.
GN MLR5043.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
[1]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=NAFF303099;
RX KANeko T., NAKamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).

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EMBL; AF003005; BAB51560.1; -.
GO; GO:0005224; F-ATP binding; IEA.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0004812; F:RNA ligase activity; IEA.
GO; GO:0006418; P:amino acid activation; IEA.
GO; GO:0009152; P:metabolism; IEA.
InterPro; IPR003781; CoA-binding.
InterPro; IPR005811; CoA-ligase.
InterPro; IPR001412; tRNA-synt_1.
Pfam; PF02629; CoA binding; 1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
KW Hypothetical protein; Complete proteome.
SEQUENCE 694 AA, 73125 MW, 19E497853IDCF6CC CRC64;

Query Match          16.4%; Score 82.5; DB 16; Length 694;
Best Local Similarity 33.3%; Pred.No. 25;
Matches 33; Conservative 11; Mismatches 42; Indels 13; Gaps 4;

              3 LAALGLCVALSCTSSAAAFVNGS-AKVPQPVVALESAAEAAGTLPANPGTLNP-----L 57
              :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
438 MVPLFGISAMDAAGAAGAAFIGWAWAEPPQAQVDVT--SAAGAAGG-----GHYTPDEAEA 489
              :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

              58 KLLLSLGLGVNHLIEGSQKVAVELGPQAVGAVKALKAL 96
              :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
490 KARLIKAGLVPVKGERAGNAVAVETISSMAIGFFVALKAL 528
              :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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RESULT 6
Q9SU83
PRELIMINARY; PRT; 496 AA.
Q9SU83
(TrEMBLrel. 13, Created)
01-MAY-2000
(TrEMBLrel. 13, Last sequence update)
01-MAY-2000
(TrEMBLrel. 25, Last annotation update)
01-OCT-2003
Nucleotide nucleosencatcatcalkalike nrateis (572 nt)

DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR000515; BPD\_transp.  
DR Pfam; PF00528; BPD\_transp; 2.  
KW Complete proteome.  
SQ SEQUENCE 601AA; 61216 MW; 78

Query Match 15.4%; Score 77.5; DB 16; Length 601;  
Best Local Similarity 30.7%; Pred. No. 63;  
Matches 42; Conservative 10; Mismatches 48; Indels 37

QY	3	LAALIGLGV	ALSCSAAFLV	GSAA--KPVA-----	OPVALESAAEAGAG-----	45
Db	426	LVALLVTAV	AGSAAATPAL	AVAGVAVAPLA	AHTSSLLRQERATHITAT	TGGLGAGPVHLL 485
QY	46	-----	TLANPLGTL	NPLKLLSSLGI-----	PVNHTEGSKCV	VAELGPQ 85
Db	486	RHEILLPA	VVPVLRHALL	RLPGVAAALAS	IGFLGAGPPSP	EWGLLLANOPYASRAPW 545

RA EU Arabidopsis sequencing project;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

[3] RP SEQUENCE FROM N.A.  
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[4] RN

RA EU Arabidopsis sequencing project;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL079344; CAB45328.1; -  
DR EMBL; AL161575; CAB79726.1; -  
DR PIR; T09931; T09931.

DR	GO; GO:0015787; F:hydrolase activity; IEA.
DR	GO; GO:0004551; F:nucleotide diphosphatase activity; IEA.
DR	GO; GO:0009117; F:nucleotide metabolism; IEA.
DR	InterPro: IPR002591; P:phosphodiester.
DR	Pfam: PF01663; P:phosphodiester; 1.
KW	Hydrolase.
DR	SEQUENCE 496 AA; 54678 MW; 8DC2B4346121D732 CRC64;

Query Match 16.1%; Score 81; DB 10; Length 496;  
Best Local Similarity 41.3%; Pred. No. 24;  
Matches 26; Conservative 14; Mismatches 17; Indels 6; Gaps 3;

6 LLGLCVALSCSAAAFVLSGSAKVPVAALESAAEAGA--GTLANPLGTIN-PLKLLLS 62

57 LLVTCIALSASAFAPLFFSSQ---KPVLSLNOISKSPAFDRSVARPLKLDKPVVLLS 113

QY	63	SLG	65
Db	114	SDG	116

RESULT 7  
Q8XW23  
ID Q8XW23  
PRELIMINARY: PRT. 148 AD

01-NAR-2002 (TrEMBLrel. 20, Created)  
DT  
01-NAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT  
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)  
DT  
DE Probable lipoprotein.  
DE  
RSC2652 OR RS04564.  
GN  
Ralstonia solanacearum (Pseudomonas solanacearum).  
OC  
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Ralstonia.  
OC NCBI Taxid:305;

[11]  
SEQUENCE FROM N.A.  
STRAIN=CM11000;  
MEDLINE=21681879; PubMed=11823852;  
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange  
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,  
Weissenbach J., Boucher C.A.;  
"Genome sequence of the plant pathogen *Ralstonia solanacearum*."  
Nature 415:497-502(2002).



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:05:19 ; Search time 4.04538 Seconds  
(without alignments)

1338.637 Million cell updates/sec

Title: US-09-700-770-9

Perfect score: 502

Sequence: 1 MKLALLGLCVLSCSSAAA.....QAVGAVKALKALGALTVFG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	497	99.0	104	UGR2_HUMAN	Q96qr1 homo sapien
2	250	49.8	104	UGR2_MOUSE	Q920q7 mus musculus
3	160	31.9	93	UGR1_HUMAN	Q96p11 homo sapien
4	135	26.9	139	UGR1_MOUSE	Q920h1 mus musculus
5	83	16.5	1327	TRK1_HUMAN	Q95271 homo sapien
6	77	15.3	335	TRK2_STRCO	Q924w9 streptomyce
7	76	15.1	732	COPA_HELPFE	Q32619 helicobacte
8	75	14.9	362	MDC1_HUMAN	Q9h1k6 homo sapien
9	75	14.9	362	MDC1_MOUSE	Q9ere8 mus musculus
10	74	14.7	779	SN1L_MOUSE	Q60670 mus musculus
11	73.5	14.6	626	DXS_WIGBR	Q8d357 wigglsworth
12	73.5	14.6	776	SN1L_RAT	Q9r1u5 rattus norv
13	73.5	14.6	882	SYA_THETH	P74941 theromus the
14	72	14.3	397	SUCC_AGR5	Q8uc60 agrobacteri
15	71	14.1	428	FXB2_MOUSE	G64733 mus musculus
16	71	14.1	480	DNAH_RHIME	P35890 rhizobium m
17	69	13.7	124	RL7_RALSO	Q8xuz7 ralstonia s
18	68.5	13.6	377	PROB_BIFLO	Q8g4t9 bifidobacte
19	68	13.5	334	PEPD_ECOLI	P23876 escherichia
20	68	13.5	569	SILF_MOUSE	Q920q3 mus musculus
21	67.5	13.4	2035	Y233_HUMAN	Q92508 homo sapien
22	67	13.3	331	GCP_MYCLE	P37969 mycobacteri
23	67	13.3	464	FUMC_PSESM	Q885v0 pseudomonas
24	66.5	13.2	341	TA2R_RAT	P34978 rattus norv
25	66.5	13.2	465	FXD1_HUMAN	Q16676 homo sapien
26	66	13.1	118	NLTD_BRAOL	Q43304 brassica ol
27	66	13.1	121	NP70_MYCKA	Q49614 mycobacteri
28	66	13.1	239	CLRC_IDEDE	P60000 ideonella d
29	66	13.1	527	PTB_MOUSE	P17225 mus musculus
30	66	13.1	540	LEU1_PROMM	Q7tuy5 prochloroco
31	66	13.1	585	NUPI_RAT	P70581 rattus norv
32	65.5	13.0	257	EUTC_RHOER	Q59782 rhodococcus
33	65.5	13.0	336	COB1_RHILLO	Q98kn9 rhizobium l

34	65.5	13.0	491	1	Y084_MYCTU	O53209 mycobacteri
35	65	12.9	344	1	TRD2_RALSO	Q8x800 ralstonia s
36	65	12.9	399	1	YM96_SYNEL	Q8gdm0 synechococc
37	65	12.9	462	1	AZAC_HUMAN	P18825 homo sapien
38	65	12.9	693	1	RECG_ECOLI	P24230 escherichia
39	65	12.9	4377	1	ANK3_HUMAN	Q12955 homo sapien
40	64.5	12.8	184	1	CYCM_BRAJA	P30323 bradyrhizob
41	64.5	12.8	320	1	Y678_METJA	Q58091 methanococc
42	64.5	12.8	750	1	ELS_CHICK	P07916 gallus gall
43	64.5	12.8	905	1	NUOG_PSEAE	Q9i0j6 pseudomonas
44	64.5	12.8	1023	1	RT11_ACTPL	P55128 actinobacil
45	64.5	12.8	1023	1	RT12_ACTPL	P55129 actinobacil

#### ALIGNMENTS

RESULT :  
UGR2\_HUMAN  
ID UGR2\_HUMAN STANDARD; PRT; 104 AA.  
AC Q96QR1; Q96PL0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in normal-1) (Secretoglobin family 3A member 1).  
GN SCGB3A1 OR UGRP2 OR HIN1.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21396515; PubMed=11481438;  
RA Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P., Kaelin C.M., Rhei E., Rosenberg M., Schnitt S., Marks J.R., Pagon Z., Belina D., Razumovic J., Polyak K.;  
RT "HIN-1, a putative cytokine highly expressed in normal but not cancerous mammary epithelial cells";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).  
[2]  
SEQUENCE FROM N.A.  
RP MEDLINE=21539178; PubMed=11682631;  
RX Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., Kimura S.;  
RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor";  
RL Mol. Endocrinol. 15:2021-2036(2001).  
CC -!- FUNCTION: Potential growth inhibitory cytokine.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Highly expressed in breast tissues. Absent in breast cancer cell lines.  
CC -!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.  
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CC -----  
DR EMEL; AF040564; AAK82942.1; -;  
DR EMEL; AF13458; AAL26217.1; -;  
DR Gerew; HGNC:18384; SCGB3A1.  
DR MIM; 606500; -;  
DR GO; GO:0003576; C:extracellular; NAS.  
DR GO; GO:0005125; P:cytokine activity; NAS.  
DR GO; GO:0003080; P:negative regulation of cell growth; NAS.  
DR GO; GO:0042127; P:regulation of cell proliferation; NAS.  
DR Cytokine; Signal.  
FT SIGNAL 1 20 POTENTIAL.



FT	VAHSPLIC	107	139	VSUFLPMICAYPRDSKQQTAFIERVEQSKL -> EALS
FT	FT			HLV (in isoform B).
FT	FT			/FTid=VSP_006726.
FT	VAHSPLIC	85	91	VIIICSY -> EALSHLV (in isoform A).
FT	FT			/FTid=VSP_006727.
FT	VAHSPLIC	92	139	Missing (in isoform A).
FT	FT			/FTid=VSP_006728.
SEQ	SEQUENCE	139 AA;	15431 MW;	8A2FH080B41B65E4 CRC64;
Query Match				
Best local Similarity		26.9%; Score 135; DB 1; Length 139;		
Matches		34; Conservative 17; Mismatches 36; Indels 10; Gaps 1		
QY	1	MKLAALLGLCVALS	SSAAFLVGS	AKPVAQFPVALESAAEAGAGTLANPIGTLNPKLL 60
DB	1	MKLVISIFLLVTIG	CGYSATALLNRLFLVVDKLFV-----	PLDDIIIPSPDLKWL 50
QY	61	LSLIGLIPVNHLEIG	SQKCVAEIGLGPQAVGAVKALKALL 97	
DB	51	LKTIGISVEHLVTG	LKKCVDELGPSEAEVKKLLVII 87	
RESULT 5				
TNKL	HUMAN	STANDARD;	PRT;	1327 AA.
ID	AC	O95271;	O95272;	
DT	28-FEB-2003	(Rel. 41, Created)		
DT	28-FEB-2003	(Rel. 41, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Tankyrase 1 (EC 2.4.2.30) (TANK1) (Tankyrase 1) (TNKS-1) (TRF1-			
DE	interacting ankyrin-related ADP-ribose polymerase).			
OS	TNKS OR TNKS1 OR TN1 OR TNF1 OR PARPL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI	Taxid:9606;			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TIGSUB=Testis;			
RC	MEDLINE=99040105; PubMed=98232378;			
RA	Smith S., Gariat I., Schmitt A., de Lange T.;			
RA	"Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";			
RL	Science 282:1484-1487(1998).			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TIGSUB=Testis;			
RC	MEDLINE=99040105; PubMed=98232378;			
RA	Smith S., de Lange T.;			
RA	"Cell cycle dependent localization of the telomeric PARP, tankyrase,			
RT	to nuclear pore complexes and centrosomes.";			
RL	J. Cell Sci. 112:3649-3656(1999).			
RP	FUNCTION, AND PHOSPHORYLATION.			
RP	MEDLINE=20556282; PubMed=10988299;			
RA	Chi N.-W., Lodish H.F.;			
RA	"Tankyrase is a Golgi-associated mitogen-activated protein kinase			
RT	substrate that interacts with IRAP in GLUT4 vesicles.";			
RL	J. Biol. Chem. 275:38437-38444(2000).			
RP	FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.			
RP	MEDLINE=21602874; PubMed=11739745;			
RA	Cook B.D., Dymek J.N., Chang W., Shostak G., Smith S.;			
RT	"Role for the related poly(ADP-ribose) polymerases tankyrase 1 and 2			
RT	at human telomeres.";			
RL	Mol. Cell. Biol. 22:332-342(2002).			
CC	-I- FUNCTION: May regulate vesicle trafficking and modulate the			
CC	subcellular distribution of SLC2A4/GLUT4-vesicles. Has PARP			
CC	activity and can modify TRF1, and thereby contribute to the			
CC	regulation of telomere length.			
CC	-I- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribose} (N)-acceptor =			
CC	nicotinamide + {ADP-D-ribose} (N+1)-acceptor.			
CC	-I- SUBUNIT: Oligomerizes and associates with TNKS2. Interacts with			
CC	the cytoplasmic domain of LNPEP/Otaase in SLC2A4/GLUT4-vesicles.			
CC	binds to the N-terminus of telomeric TRF1 via the ANK repeats			



DR	TIGFPMs; TIGR01525; ATPase-IB bVv; 1.
DR	TIGFPMs; TIGR01494; ATPase_P-Type; 3.
DR	PROSITE; PS00154; ATPase_E1_E2; 1.
DR	PROSITE; PS01047; HWA_1; 1.
DR	PROSITE; PS0846; HWA_2; 1.
KW	Transport; Ion transport; Copper transport; Hydrophobic; ATP-binding;
KW	Metal-binding; Copper; Magnesium; Transmembrane; Phosphorylation.
FT	CYTOPLASMIC (POTENTIAL).
DOMAIN	1 88
FT	POTENTIAL.
FT	TRANSMEM 89 109
DOMAIN	110 122
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	TRANSMEM 123 142
DOMAIN	143 149
FT	CYTOPLASMIC (POTENTIAL).
FT	POTENTIAL.
FT	TRANSMEM 150 170
DOMAIN	171 187
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	TRANSMEM 188 208
DOMAIN	209 336
FT	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 337 359
DOMAIN	360 365
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	TRANSMEM 366 383
DOMAIN	384 663
FT	CYTOPLASMIC (POTENTIAL).
FT	POTENTIAL.
FT	TRANSMEM 664 683
DOMAIN	684 694
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	TRANSMEM 695 713
DOMAIN	714 732
FT	CYTOPLASMIC (POTENTIAL).
FT	HMA.
FT	MOD RES 3 69
FT	PHOSPHORYLATION (BY SIMILARITY).
FT	COPPER (POTENTIAL).
FT	METAL 13 13
FT	COPPER (POTENTIAL).
FT	METAL 16 16
FT	MAGNESIUM (BY SIMILARITY).
FT	METAL 609 609
FT	MAGNESIUM (BY SIMILARITY).
FT	METAL 613 613
SEQUENCE	732 AA; 78853 MW; 7105107EA5949EFD CRC64;
QY	Query Match 15.1%; Score 76; DB 1; Length 732;
Db	Best local similarity 26.3%; Pred. No. 16; Gaps 6
Matches	35; Conservative 17; Mismatches 39; Indels 42; Gaps 6
QY	6 LLGLCVALS...AAFLVGSAPKPVPAAL-----ESAAEAGAG-----45
Db	447 LTLTCLASLEAQSEHVIAGIVAHAKEGQIALQEVOVKPGFKGVGDPQIIKAGNLE 506
QY	46 --TANPLGTLPKLKLLS----LGIPV--NHLEGGSKCVAEELGPQAVCA-----89
Db	507 FFNLNPFPTLEGIQVFVTETQILGVVVVLDSLKEGSKAISEL--KAUGVKTLLSGD 564
QY	90 ----VKALKALG 98
Db	565 NLNVRLATQLG 577
RESULT B	
MDCL_HUMAN	
ID MDCL_HUMAN STANDARD; PRT; 362 AA.	
AC Q9HIK6;	
DT 28-FEB-2003 (Rel. 41, Created)	
DT 28-FEB-2003 (Rel. 41, Last sequence update)	
DT 28-FEB-2003 (Rel. 41, Last annotation update)	
DE Mesoderm development candidate 1.	
GN MESDC1.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RC SEQUENCE FROM N.A.	
RP TISSUE=Retina;	
RX MEDLINE=21145589; PubMed=11247670;	
RA Winee M.E., Lee L., Katari M.S., Zhang L., DeRossi C., Shi Y.,	
RA Perkins S., Ralzman M., McCombie W.R., Holdener B.C.;	
RT Identification of mesoderm development (mesd) candidate genes by	
RT comparative mapping and genome sequence analysis."	
RL Genomics 72:88-98(2001).	
CC -! SIMILARITY: SOME, TO TALIN.	



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DR EMBL; AY007810; AAG41058.1; -;  
 DR Genew; HGNC:13519; MESDC1.  
 SQ SEQUENCE 362 AA; 37758 MW; 37BF391D663E1D6E CRC64;

Query Match 14.9%; Score 75; DB 1; Length 362;  
 Best Local Similarity 35.4%; Pred. No. 11;  
 Matches 28; Conservative 6; Mismatches 33; Indels 12; Gaps 3;  
 QY 3 LAALGLCVALS-CSSAAAFVGSAPVQAP-----VALESAAEAGAGTL-ANP 50  
 DB 112 LVELGDLVSLTECSAAAYLAAVATPGAPQGLVDYRVTTCRHEVEQGCAVLATP 171  
 QY 51 LGTINPLKLLSSLGIPVN 69  
 DB 172 LADMTPLLEVSQGLSRN 190

RESULT 9  
 MDC1\_MOUSE  
 ID MDC1\_MOUSE STANDARD; PRT; 362 AA.  
 AC Q9ERB8;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Mesoderm development candidate 1.  
 GN MESDC1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RC STRAIN=129/SVJ;  
 RX MEDLINE=21145589; PubMed=11247670;  
 RA Wines M.E., Lee L., Katari M.S., Zhang L., DeRossi C., Shi Y.,  
 RA Perkins S., Feldman M., McCombie W.R., Holdener B.C.;  
 RA "Identification of mesoderm development (mesd) candidate genes by  
 RT comparative mapping and genome sequence analysis.";  
 RL Genomics 72:88-98(2001).  
 RN [2]

SEQUENCE FROM N.A.  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kattaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- TISSUE SPECIFICITY: Ubiquitous.  
 CC -!- SIMILARITY: SOME, TO TALIN.

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DR EMBL; AF311213; AAG33620.1; -;  
 DR EMBL; BC018326; AAH18326.1; -;  
 DR MGD; MGI:1891420; Mesdcl.  
 SQ SEQUENCE 362 AA; 37786 MW; EFE9BBFC09BB7CBS CRC64;

Query Match 14.9%; Score 75; DB 1; Length 362;  
 Best Local Similarity 35.4%; Pred. No. 11;  
 Matches 28; Conservative 6; Mismatches 33; Indels 12; Gaps 3;  
 QY 3 LAALGLCVALS-CSSAAAFVGSAPVQAP-----VALESAAEAGAGTL-ANP 50  
 DB 112 LVELGDLVSLTECSAAAYLAAVATPGAPQGLVDYRVTTCRHEVEQGCAVLATP 171  
 QY 51 LGTINPLKLLSSLGIPVN 69  
 DB 172 LADMTPLLEVSQGLSRN 190

RESULT 10  
 SNIL\_MOUSE  
 ID SNIL\_MOUSE STANDARD; PRT; 779 AA.  
 AC Q60670;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Probable serine/threonine protein kinase SNF1K (EC 2.7.1.-) (HRT-20)  
 DE (Myocardial SNF1-like kinase).  
 GN SNF1K OR MSK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND REVISIONS TO 8; 16-18; 44-45; 316 AND 435.  
 RC TISSUE=Embryo;  
 RA Ruiz J.C.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 1-435 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Embryo;  
 RX MEDLINE=95200798; PubMed=7893599;  
 RA Ruiz J.C., Conlon F.L., Robertson E.J.;  
 RA "Identification of novel protein kinases expressed in the myocardium  
 RT of the developing mouse heart.";  
 RL Mech. Dev. 48:153-164(1994).  
 CC -!- TISSUE SPECIFICITY: Expressed in lung, skin, ovary, heart and  
 CC stomach. No expression in brain, liver or skeletal muscle.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 1 UBA domain.

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DR EMBL; U11494; AAA67926.2; -;  
 DR HSSP; P24941; 1AQL.  
 DR MGD; MGI:104754; Snf1lk.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.



```

DR InterPro; IPR001245; Tyr kinase.
DR InterPro; IPR000449; UBA domain.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00300; UBA; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 27 278 PROTEIN_KINASE.
FT BIND 303 343 UBA.
FT NP_BIND 33 41 ATP (BY SIMILARITY).
FT BINDING 56 56 ATP (BY SIMILARITY).
FT ACT_SITE 149 149 BY SIMILARITY.
SQ SEQUENCE 773 AA; 85027 MW; 7B08131BC46D9C4E CRC64;

Query Match 14.7%; Score 74; DB 1; Length 779;
Best Local Similarity 32.9%; Pred. No. 26;
Matches 26; Conservative 11; Mismatches 30; Indels 12; Gaps 3;

QY 10 CVALSCSAAALVGSAPVQPVAALESAAAGAGTLANP--LGTLPKLLKLLSSLGHP 67
DB C I V S S A T A S E S G T S D C L P F S A S E G P A G L G S G - L A T P G L L G T S P V R L A S P F L - - - - 545

QY 68 VNHLEGGQKCVAEILGPQA 86
DB 546 -----GQSATPVLQTQA 558

RESULT 11
DXX_WIGBR
ID DXX_WIGBR STANDARD; PRT; 626 AA.
AC Q8D357;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1-deoxy-D-xylose-5-phosphate synthase (EC 2.2.1.7) (1-deoxyxylose-5-phosphate synthase) (DXP synthase) (DXPS).
GN DXP OR WIGBR1440.
OS Wigglesworthia glossinidia brevipalpis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Wigglesworthia.
OX NCBI_TaxID=36870;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=22297718; PubMed=12219091;
RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M., Aksoy S.;
RT "Genome sequence of the endocellular obligate symbiont of tsetse flies, Wigglesworthia glossinidia.";
RL Nat. Genet. 32:402-407(2002).
CC -!- FUNCTION: Catalyzes the acyloin condensation reaction between C atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylose-5-phosphate (DXP) (By similarity).
CC -!- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-deoxy-D-xylose-5-phosphate + CO(2).
CC -!- COFACTOR: Binds 1 thiamine pyrophosphate per subunit (By similarity).
CC -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; first step.
CC -!- PATHWAY: Biosynthetic pathway to thiamine and pyridoxol; first step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
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CC EMBL; AB063521; BAC24290.1; -.
DR HAMAP; MF_00315; -, 1.
DR InterPro; IPR005477; Dxe_synth.
DR InterPro; IPR009014; Transketo_C_like.
DR InterPro; IPR005476; Transketolase_C.
DR InterPro; IPR005475; Transketolase_CR.
DR InterPro; IPR005474; Transketolase_N.
DR Pfam; PF02779; transket_pyz; 1.
DR Pfam; PF02780; transketolase_C; 1.
DR TIGRFAMs; TIGR00204; dxs; 1.
DR PROSITE; PS00801; TRANSKETOLASE_1; 1.
DR PROSITE; PS00802; TRANSKETOLASE_2; FALSE NEG.
KW Transferase; Flavoprotein; Thiamine pyrophosphate;
KW Isoprene biosynthesis; Thiamine biosynthesis; Complete proteome.
SQ SEQUENCE 626 AA; 69851 MW; C77008D2D82ABE21 CRC64;

Query Match 14.6%; Score 73.5; DB 1; Length 626;
Best Local Similarity 30.0%; Pred. No. 24;
Matches 24; Conservative 14; Mismatches 41; Indels 1; Gaps 1;

QY 22 LVGSNAKPVQPVAALESAAAGAGTLANPLGTLPKLLKLLSSLGTPVNHLEGGQKCV-A 80
DB L I R M A K T H K A L I T T E N V I M G G A S V A N F I M Y N K L L V P L N I G I P D N F V S H G S Q T E V R S 605

QY 81 ELGPOAVGAVKALKALGAL 100
DB 606 SLGLDSIGIKKIKNWLNFL 625

RESULT 12
SNIL_RAT
ID SNIL_RAT STANDARD; PRT; 776 AA.
AC Q9RIJ5; Q9R081;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine protein kinase SNFILK (EC 2.7.1.-) (Salt-inducible protein kinase) (protein kinase KID2).
GN SNFILK OR SIK OR KID2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
RX MEDLINE=99330184; PubMed=10403390;
RA Wang Z., Takemori H., Halder S.K., Nonaka Y., Okamoto M.;
RT "Cloning of a novel kinase (SIK) of the SNF1/AMPK family from high salt diet-treated rat adrenal.";
RL FEBS Lett. 453:135-139(1999).
RN [2]_
RP SEQUENCE FROM N.A.
RA Feldman J.D., Vician L., Crispino M., Hoe W., Baudry M., Herschman H.R.;
RT "The KID2 gene encodes a protein kinase induced by depolarization in brain.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1 subfamily.
CC -!- SIMILARITY: Contains 1 UBA domain.
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CC EMBL; AB020480; BAAG2673.1; -.
DR EMBL; AF106937; AAF14191.1; -.

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DR HSP: P24941; 13Q1.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR000449; UBA domain.
DR Pfam; PF00069; pkinae; 1.
DR ProDom; PD000001; S TKC; 1.
DR SMART; SM00220; S TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00300; UBA; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 27 278 PROTEIN KINASE.
FT DOMAIN 303 343 UBA.
FT NP_BIND 33 41 ATP (BY SIMILARITY).
FT BINDING 56 56 ATP (BY SIMILARITY).
FT ACT_SITE 149 149 BY SIMILARITY.
FT CONFLICT 473 473 R -> K (IN REF. 2).
SQ SEQUENCE 776 AA; 84908 MW; 7BF745AF28F17E6E CRC64;

Query Match 14.6%; Score 73.5; DB 1; Length 776;
Best Local Similarity 33.7%; Pred. No. 28;
Matches 28; Conservative 11; Mismatches 31; Indels 13; Gaps 4;

QY 10 CVALSCSSAAFLVGSAPVAPVAALESAAEAGAGTLANP--LGTLPKLLSLGIP 67
DB 490 CLIVSSAAVSEGTSSDSCLPFASGEPAGLGG-LATPGLLTGTSFVRLASPLF--- 545

QY 68 VNHLEGSQKCAELGPQA-VGA 89
DB 546 -----GSGSATPVLQSQAGLGA 562

RESULT 13
SYA_TETH STANDARD; PRT; 882 AA.
AC P74941;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine-tRNA ligase) (Alars).
GN ALAS.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OC NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=97351141; PubMed=9207019;
RA Lechler A., Martin A., Zuleeg T., Limmer S., Kreutzer R.;
RT "A biologically active 53 kDa fragment of overproduced alanyl-tRNA synthetase from Thermus thermophilus HB8 specifically interacts with tRNA ala acceptor helix.";
RL Nucleic Acids Res. 25:2737-2744 (1997).
CC -!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP + diphosphate + L-alanyl-tRNA(Ala).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC
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CC -----
CC EMBL; Y08363; CAA69650.1; -.
DR HAMAP; MF_00036; -.
DR InterPro; IPR003156; DHHA1.
DR InterPro; IPR002318; tRNA-synt_2c.

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DR InterPro; IPR006193; tRNA_synt_Ala.
DR Pfam; PF02272; DHHA1; 1.
DR Pfam; PF01411; tRNA-synt_2c; 1.
DR PRINTS; PR00980; TRNASYNTHALA.
DR TIGRFAMs; TIGR00344; alas; 1.
DR PROSITE; PS50860; AA tRNA LIGASE II ALA; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SQ SEQUENCE 882 AA; 97454 MW; E50E3E34480CFC56 CRC64;

Query Match 14.6%; Score 73.5; DB 1; Length 882;
Best Local Similarity 32.6%; Pred. No. 32;
Matches 30; Conservative 12; Mismatches 47; Indels 3; Gaps 2;

QY 6 LLGLCVALSASSAAFLVGSAPVAPVAALESAAEAGAGTLANPLGTLNPKLLSLG 65
DB 681 LCGGCHVRRGTGEGAFILRSEAVSAGVRRIE--AVTGEAIRFARGSLNKLALAE 738

QY 66 IPVNHLEGSQKCAELGPQA-VGA 97
DB 739 VGEAALERLEKLLAEL-KEXEREVESLKARL 769

RESULT 14
SUCC_AGR5 STANDARD; PRT; 397 AA.
ID SUCC_AGR5 STANDARD; PRT; 397 AA.
AC Q8UC60;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Succinyl-CoA synthetase beta chain (EC 6.2.1.5) (SCS-beta).
SUCC OR ATU2638 OR AGR_C4780.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OC NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutaydin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens C58.";
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goddard B., Hinkle G., Gattung S., Miller N., Blanchard M., Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Roumel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Planagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328 (2001).
CC -!- CATALYTIC ACTIVITY: ATP + succinate + CoA = ADP + succinyl-CoA + phosphate.
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SUBUNIT: Composed of an alpha chain and a beta chain (By similarity).
CC -!- SIMILARITY: Belongs to the succinate/malate CoA ligase beta subunit family.
CC
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CC EMBL; AE009211; AAL43619.1; -
CC EMBL; AE008177; AAK83359.1; -
CC PIR; AE2900; AE2900.
CC PIR; F97675; F97675.
CC HANAP; MF_00558; -; 1.
CC InterPro; IPR003135; ATP-grasp.
CC InterPro; IPR005809; CoA lig beta.
CC InterPro; IPR005811; CoA_ligase.
CC Pfam; PF02222; ATP-grasp; 1.
CC Pfam; PF00549; ligase-CoA; 1.
CC TIGRFAMs; TIGR01016; succCoabeta; 1.
CC PROSITE; PS01217; SUCCINYL COA LIG 3; FALSE NEG.
KW Ligase; Tricarboxylic acid cycle; Complete proteome.
SQ SEQUENCE 397 AA; 41899 MW; 223CIA3825764F9F CRC64;

Query Match 14.3%; Score 72; DB 1; Length 397;
Best Local Similarity 36.2%; Pred. No. 21;
Matches 29; Conservative 8; Mismatches 31; Indels 12; Gaps 4;

QY 18 AARLVGSAPQVAPVALE-SAAEAGAGTIANPLGTINPLKLLSLGIPVNHLEGSQ 76
DQ 8 AKALLKGGVAGVAVGAILKVEEAARAAKQIPGLYV---VKSOIHAGG-----RGKG 57
QY 77 KCVAEIQLPQAVGAVKALKAL 96
DQ 58 K-FKELGPDAGGVRLAKSI 76

RESULT 15
ID_FXB2_MOUSE STANDARD; PRT; 428 AA.
AC Q64733;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Forkhead box protein B2 (Transcription factor FKX-4).
GN FOXB2 OR FKX4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97014266; PubMed=8861101;
RA Kaestner K.H., Schuetz G., Monaghan A.P.;
RT "Expression of the winged helix genes fkh-4 and fkh-5 defines domains
RT in the central nervous system.";
RL Mech. Dev. 55:221-230(1996).
RN [2]
RP SEQUENCE OF 4-114 FROM N.A.
RC STRAIN=129;
RX MEDLINE=93361500; PubMed=7689224;
RA Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H.,
RA Monaghan A.P., Schuetz G.;
RT "Six members of the mouse forkhead gene family are developmentally
RT regulated.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631(1993).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: Expressed during embryogenesis.
CC -!- SIMILARITY: Contains 1 fork-head domain.
CC
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CC -----
CC EMBL; X92591; CAA63335.1; -
CC EMBL; X71942; CAA50744.1; -
CC PIR; D47746; D47746.
CC HSP; Q63245; 2HFH.
CC TRANSFAC; T02442; -
CC MCD; MGI.1347468; Foxb2.
CC InterPro; IPR001766; TF_Fork_head.
CC Pfam; PF00250; Fork_head; 1.
CC PRINTS; PR00053; FORKHEAD.
CC ProDom; PD000425; TF_Fork_head; 1.
CC SMART; SM00339; FH; 1.
CC PROSITE; PS00657; FORK_HEAD_1; 1.
CC PROSITE; PS00658; FORK_HEAD_2; 1.
CC PROSITE; PS00039; FORK_HEAD_3; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
FT DNA_BIND 12 103 FORK-HEAD.
FT DOMAIN 139 153 POLY-HIS.
FT DOMAIN 156 162 POLY-HIS.
FT DOMAIN 163 172 POLY-PRO.
FT DOMAIN 217 231 POLY-ALA.
FT DOMAIN 249 258 POLY-ALA.
FT DOMAIN 321 330 POLY-ALA.
FT DOMAIN 396 399 POLY-ALA.
SQ SEQUENCE 428 AA; 45170 MW; DB8A8EFD1E94AB10 CRC64;

Query Match 14.1%; Score 71; DB 1; Length 428;
Best Local Similarity 29.2%; Pred. No. 28;
Matches 33; Conservative 17; Mismatches 43; Indels 20; Gaps 6;

QY 11 VALSCSSAAAFVGSAPKPAQ-PVAALSAEAGAGTIANPLGTINPL-----KL 59
DQ 220 VAAAAAARAAAVGVGRLSQFPYPYGLGSAARAAAAAATGFKHFAHNIIGRDYKG 279
QY 60 LLSSLGIP----VNHL----IEGS-QKCVAEIQLPQAVGAVKALKALLGALTYFG 104
DQ 280 VLAQAGGLPLASVMHILGYPVPGQLSNVGVSWPH-VGVMDSVAAAAAAG 331

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Search completed: June 2, 2004, 20:19:36  
Job time : 5.04538 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 20:14:10 ; Search time 7.07942 Seconds  
(without alignments)  
1413.099 Million cell updates/sec

Title: US-09-700-770-9  
Perfect score: 502  
Sequence: 1 MKLAALGLCVLSCSSAAA.....QAVGAVKALKALLGALTAVFG 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	16.1	496	2 T09931	probable phosphodiesterase I
2	79.5	15.8	1381	2 S60004	hypothetical prote
3	77.5	15.4	601	2 T35054	probable transport
4	77	15.3	335	2 T36304	probable anthranil
5	76	15.1	355	2 AD2973	hypothetical prote
6	76	15.1	355	2 G98309	probable ABC trans
7	76	15.1	699	2 H87275	thio-disulfide int
8	76	15.1	732	2 T47269	copper-transportin
9	75.5	15.0	544	2 H72647	hypothetical prote
10	73.5	14.6	331	2 C84358	transport protein
11	73	14.5	502	2 F83553	probable aldehyde
12	73	14.5	584	2 B87315	gamma-glutamyltran
13	73	14.5	1279	2 T13613	hypothetical prote
14	72	14.3	236	2 A52010	amaatigote-specifi
15	72	14.3	397	2 AE2900	succinyl-CoA synth
16	72	14.3	397	2 F97675	succinyl-CoA synth
17	72	14.3	528	2 D70968	hypothetical prote
18	71.5	14.2	462	2 B87634	L-serine dehydrata
19	71.5	14.2	874	2 AC3070	ATP-dependent Clp
20	71.5	14.2	887	2 F98216	endopeptidase clp
21	71	14.1	440	2 C83368	probable MPS trans
22	70.5	14.0	668	2 G85160	heat shock protein
23	70.5	14.0	831	2 D71409	probable endopepti
24	70	13.9	431	2 C86178	hypothetical prote
25	70	13.9	452	2 T46147	zinc finger protei
26	70	13.9	477	2 D82179	probable multidrug
27	69.5	13.8	244	2 S75653	hypothetical prote
28	69.5	13.8	396	2 D75454	hypothetical prote
29	69.5	13.8	423	2 C70582	probable PPE prote

30	69.5	13.8	455	2 AD0782	probable L-serine
31	69	13.7	170	2 AF3312	hypothetical prote
32	69	13.7	627	2 D75393	serine proteinase,
33	69	13.7	853	2 T36551	probable ATP-depen
34	69	13.7	3295	2 AF0074	probable adhesin Y
35	68.5	13.6	277	2 F84336	hypothetical prote
36	68.5	13.6	335	2 AB0575	ferric enterobacti
37	68.5	13.6	1724	2 T18343	p-glycoprotein - S
38	68	13.5	334	2 S16296	ferric enterobacti
39	68	13.5	334	2 A85558	ferric enterobacti
40	68	13.5	334	2 E90707	ferric enterobacti
41	67.5	13.4	560	2 F70719	hypothetical prote
42	67.5	13.4	387	2 C75312	branched-chain ami
43	67.5	13.4	1179	2 H82706	hypothetical prote
44	67.5	13.4	1206	2 B87247	probable conserved
45	67.5	13.4	2698	2 B96671	similar to transla

## ALIGNMENTS

### RESULT 1

T09931  
probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T11  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Aug-2002  
C:Accession: T09931  
R:Byan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K  
submitted to the Protein Sequence Database, June 1999  
A:Reference number: Z16897  
A:Accession: T09931  
A:Molecule type: DNA  
A:Residues: 1-496 <BEV>  
A:Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T1614.190  
A:Experimental source: cultivar Columbia; BAC clone T1614  
C:Genetics:  
A:Gene: ATSP:T1614.190  
A:Map position: 4  
C:Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4  
C:Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase

Query Match	16.1%;	Score 81;	DB 2;	Length 496;
Best Local Similarity	41.3%;	Pred. No. 5.2;		
Matches	26;	Conservative	14;	Mismatches 17; Indels 6; Gaps 3;
Qy	6	LLGLCVLSCSSAAAFVGSAPVQAQPVAALESAAEAGA--GTLANPLGTLN-PLKLLLS	62	
Db	57	LLVTCLLSAASAFALFFSSQ---KPVLSLNQISKSPAFDRSVARPLKLDKPVLLIS	113	
Qy	63	SLG 65		
Db	114	SDG 116		

### RESULT 2

S60004  
hypothetical protein - common roundworm retrotransposon R4 (fragment)  
C:Species: Ascaris lumbricoides (common roundworm)  
C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 21-Jul-2000  
C:Accession: S60004  
R:Burke, W.D.; Mueller, F.; Eickbush, T.H.  
Nucleic Acids Res. 23, 4628-4634, 1995  
A>Title: R4, a non-LTR retrotransposon specific to the large subunit rRNA genes of n  
A:Reference number: S60004; MUID:96103592; PMID:8524653  
A:Accession: S60004  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1381 <BUR>  
A:Cross-references: EMBL:U29445; NID:G903660; PIDN:AAA97394.1; PID:G903661  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995  
C:Genetics:  
A:Genome: retrotransposon

Query Match 15.8%; Score 79.5; DB 2; Length 1381;  
 Best Local Similarity 27.8%; Pred. No. 20;  
 Matches 25; Conservative 15; Mismatches 23; Indels 27; Gaps 3;

QY 11 VALSCSSAAAFVLSAKVPAQVVALESAAEAGAGT-----LANPLG----- 52  
 DB 27 IAMPCTSTNFFRGPTPEPHREPTSDSLSGMSGTHRSPLNDDEVINGPKGHSDPVH 86  
 QY 53 -----TLNPLKLLSSLGIPVNHLEGSQ 76  
 DB 87 VVRAPTLHPREL---ELPIGVNLEASQ 113

RESULT 3  
 T35054  
 probable transport system permease protein - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999  
 C:Accession: T35054  
 R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, August 1998  
 A:Reference number: Z21566  
 A:Accession: T35054  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-601 <SEE>  
 A:Cross-references: EMBL:AL031371; PIDN:CAA20556.1; GSPDB:GN00070; SCOEDB:SC4G2.19  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: SCOEDB:SC4G2.19

Query Match 15.4%; Score 77.5; DB 2; Length 601;  
 Best Local Similarity 30.7%; Pred. No. 13;  
 Matches 42; Conservative 10; Mismatches 48; Indels 37; Gaps 4;

QY 3 LAALGLCVALSAAAFVLSA--KPVA-----QVVALESAAEAGAG----- 45  
 DB 426 LVALLTVNAGSAAATPALAVAGAVAPLAHTSSLLRQERATLHTATKGLGAGPVHLL 485  
 QY 46 -----TLANPLGTINPLKLLSSLGI-----PNVHLEGSQKCVAEIGPQ 85  
 DB 486 RHELLPAVVPVLRHALLRPGVALASLGLGAGPSPBPGWGLLAENQPYAERAPW 545  
 QY 86 AVCAVAKKALLGALT 102  
 DB 546 AVLAAPAAVALLGALAV 562

RESULT 4  
 T36304  
 probable antranilate phosphoribotransferase - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Jan-2000  
 C:Accession: T36304  
 R:Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, March 1999  
 A:Reference number: Z21604  
 A:Accession: T36304  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-335 <SAU>  
 A:Cross-references: EMBL:AL035654; PIDN:CAB38583.1; GSPDB:GN00070; SCOEDB:SCB8.05c  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: trpD2; SCOEDB:SCB8.05c  
 C:Superfamily: antranilate phosphoribosyltransferase; trpD homology

Query Match 15.3%; Score 77; DB 2; Length 335;  
 Best Local Similarity 34.5%; Pred. No. 8.2;  
 Matches 30; Conservative 9; Mismatches 36; Indels 12; Gaps 4;

QY 7 LGLCVALSAAAFVLSA-----KPVAQVVALESAA-----FAGAGTLANPLGTINLP 56

DB 117 LGVTRIDLGAEAAACLDRTGTITLFAVFEH--AFRHTAGPRRELGAFTVFNLLGPLCNP 174  
 QY 57 LKLLSSSLGIPVNHLEGSQKCVAEIG 83  
 DB 175 SGARLTILGVPSRELVEPMTVEVLERLG 201

RESULT 5  
 AD2973  
 hypothetical protein Atu3389 [imported] - Agrobacterium tumefaciens (strain C58, Dup  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
 C:Accession: AD2973  
 R:Wood, J.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wo  
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McC  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Ka  
 ster, E.W.  
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A:Reference number: AB2577; MUID:21608550; PMID:11743193  
 A:Accession: AD2973  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-355 <KUR>  
 A:Cross-references: GB:AE008689; PIDN:AAL44202.1; PID:gl7741781; GSPDB:GN00187  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: Atu3389  
 A:Map position: linear chromosome

Query Match 15.1%; Score 76; DB 2; Length 355;  
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QY 2 KLAALLGLCVALSAAAFVLSAKVPAQVVALESAAEAGAGTLANPLGTINPLKLL 61  
 DB 24 RILLVGLFLALCFMSAADMALGPARYTLSEVLA-----TIADPAAVGNQLRVVI 73  
 QY 62 SSLGIPVNH-----IEGSKCVA-----ELGPOAVGAVKALLGALT 103  
 DB 74 WDTRMPIALMAVTVGASLVAGAQMTILSNPLASFPTLIGISAAASFGAALAVGVGVAIF 133

RESULT 6  
 G98309  
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 C:Species: Agrobacterium tumefaciens  
 C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 18-Nov-2002  
 C:Accession: G98309  
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Golt  
 A.; Liu, F.; Wolam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,  
 Science 294, 2323-2328, 2001  
 A:Title: Genome sequence of the plant pathogen and Biotechnology Agent Agrobacterium  
 A:Reference number: A97359; MUID:21608551; PMID:11743194  
 A:Accession: G98309  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-355 <KUR>  
 A:Cross-references: GB:AE007870; PIDN:AAK90001.1; PID:gl51519970; GSPDB:GN00170  
 C:Genetics:  
 A:Gene: AGR\_L\_2865  
 A:Map position: linear chromosome

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 DB 24 RILLVGLFLALCFMSAADMALGPARYTLSEVLA-----TIADPAAVGNQLRVVI 73  
 QY 62 SSLGIPVNH-----IEGSKCVA-----ELGPOAVGAVKALLGALT 103

Db 507 FFNLPNPFLEGIQVVGTTETQILGVVVVLADSLKSGSKAISEL--KALGVKVTLLSGD 564

Qy 90 ----VKALKALLG 98  
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Db 565 NLNVRVALATQLG 577

RESULT 9

H72647  
hypothetical protein APE0614 - Aeropyrum pernix (strain K1)  
C:Species: Aeropyrum pernix  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
C/Accession: H72647  
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tera-  
awa, H.; Takamizawa, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.  
DNA Res. 6, 83-101, 1999  
A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerococcus  
A/Reference number: A72450; MUID:99310339; PMID:10382966  
A/Accession: H72647  
A>Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-544 <XAW>  
A/Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79584.1; PID:d1043370; PID:g  
A/Experimental source: strain K1  
C/Genetics:  
A/Gene: APE0614

Query Match 15.0%; Score 75.5; DB 2; Length 544;  
Best Local Similarity 26.4%; Pred. No. 18;  
Matches 33; Conservative 19; Mismatches 36; Indels 37; Gaps 5;

Qy 5 ALHLGLCVALLSCSSA-----AAFLVGSAKPVAQPVA-----LESAAEAGAGTIANP 50  
Db 18 ALVAVAVAVAAALMSVGGRTAGLIAGAGEAASQIGIAAASNPPLYMEAWVEAGA----- 71

Qy 51 LGTINPLKLLLSLGIPVNHLI-----EGSQKVSELGPQAVCAVYALK-----ALLGA 99  
Db 72 -----LKRVFSPGAPVESVVWVKPGEGVAARVELPEPAVEGVVDAMEGYDCSPVLGV 125

Qy 100 LTVFG 104  
Db 126 ETVGG 130

RESULT 10

C84358  
transport protein [imported] - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C/Accession: C84358  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laskey,  
J.; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jørgensen,  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;  
A/Title: Genome sequence of Halobacterium species NRC-1.  
A/Reference number: A84160; MUID:20504483; PMID:11016950  
A/Accession: C84358  
A>Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-331 <STO>  
A/Cross-references: GB:AEO04437; NID:g10581500; PIDN:AAG20231.1; GSPDB:GN00138  
C/Genetics:  
A/Gene: phnE

Query Match 14.6%; Score 73.5; DB 2; Length 331;  
Best Local Similarity 27.9%; Pred. No. 17;  
Matches 29; Conservative 17; Mismatches 35; Indels 23; Gaps 5;

Qy 3 LAALLGLCVALLSCSSAAAFIVLSAKPVAQPVAALSAEAGAGTIANPLGTLPKLILLS 62  
Db 83 LTSLFVGVPFDVQGYYYSFLAAHNPP-SIPLAAYETLGIATAGTV---LGA---PLALTFFG 136









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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 502; DB 9; Length 104;
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Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKLAALGLCVALSASSAAFLVGSAPVAFVVALESAAAGAGTLANPLGTINPLKLL 60
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Qy 61 LSSIGIPVNHILIESQKVAELGPQAVGAVKALKALLGALTIVFG 104
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Db 61 LSSIGIPVNHILIESQKVAELGPQAVGAVKALKALLGALTIVFG 104
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RESULT 2
US-09-989-723-408
; Sequence 408, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertschen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-10-17
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Thu Jun 3 10:25:06 2004

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;; PRIOR FILING DATE: 1998-07-09

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Db 61 LSSLGIPVNHLEIGSQKCVAEILGPOAVGAVKALKALLGALTVEG 104

RESULT 3

US-09-989-279-408  
; Sequence 408, Application US/09989279  
; Patent No. US20020072496A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Goddard, Audrey  
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; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC56  
; CURRENT APPLICATION NUMBER: US/09/989,279  
; CURRENT FILING DATE: 2001-11-19  
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; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24

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2	PRIOR FILING DATE: 1998-02-25	2	PRIOR APPLICATION NUMBER: 60/089598
3	PRIOR APPLICATION NUMBER: 60/078910	3	PRIOR FILING DATE: 1998-06-17
4	PRIOR FILING DATE: 1998-03-20	4	PRIOR APPLICATION NUMBER: 60/089599
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13	PRIOR APPLICATION NUMBER: 60/087609	13	PRIOR FILING DATE: 1998-06-18
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15	PRIOR APPLICATION NUMBER: 60/087759	15	PRIOR FILING DATE: 1998-06-18
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17	PRIOR APPLICATION NUMBER: 60/087827	17	PRIOR FILING DATE: 1998-06-19
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19	PRIOR APPLICATION NUMBER: 60/088021	19	PRIOR FILING DATE: 1998-06-19
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55	PRIOR APPLICATION NUMBER: 60/088826	55	PRIOR FILING DATE: 1998-06-25
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59	PRIOR APPLICATION NUMBER: 60/088861	59	PRIOR FILING DATE: 1998-06-25
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61	PRIOR APPLICATION NUMBER: 60/088876	61	PRIOR FILING DATE: 1998-06-25
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66	PRIOR FILING DATE: 1998-06-16	66	PRIOR APPLICATION NUMBER: 60/090863
67	PRIOR APPLICATION NUMBER: 60/089512	67	PRIOR FILING DATE: 1998-06-26
68	PRIOR FILING DATE: 19		

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 502; DB 9; Length 104;
Best Local Similarity 100.0%; Pred No. 7,5e-47; Indels 0; Gaps 0;
Matches 104; Conservative 0; Mismatches 0;

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Db 1 MKLAALLGLCVALLSCSSAAFLVGSAPVQVPAALSAEAGAGTFLANPLGTINPLKLL 60
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QY 61 LSSLGIPVNHLEGSOKVCAELGPOAVGAVKALKALLGALTVPFG 104
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RESULT 4
US-09-989-727-408
; Sequence 408, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 502; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 7.5e-47;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAALLGLCVALLSCSAAAFVLSGSAKPVAQPVAALESAAEAGAGTILANPLKLL 60
Db 1 MKLAALLGLCVALLSCSAAAFVLSGSAKPVAQPVAALESAAEAGAGTILANPLKLL 60

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Db 61 LSSLGIPVNHILIGSQKCVAEELGPOAVGVAKKALIGALTIVFG 104

RESULT 5
US-09-589-731-408
; Sequence 408, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJjavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730ELC70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1997-11-12
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; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/075945
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; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28

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69	PRIOR APPLICATION NUMBER: 60/089598
70	PRIOR FILING DATE: 1998-06-17
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72	PRIOR FILING DATE: 1998-06-17
73	PRIOR APPLICATION NUMBER: 60/089600



; PRIOR APPLICATION NUMBER: 60/091978  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 502; DB 9; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-47; Indels 0; Gaps 0;  
 Matches 104; Conservative 0; Mismatches 0;

QY 1 MKLAALLGLCVALSASAAFLVGSAPVQAPVAALLESAAEAGAGTIANPLGTINPKLL 60  
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 QY 61 LSSLGIPVNHILGSKVKVAGLGPQAVGAVKALKALIGALTVEG 104  
 Db 61 LSSLGIPVNHILGSKVKVAGLGPQAVGAVKALKALIGALTVEG 104

# RESULT 6

US-09-989-732-408  
 ; Sequence 408, Application US/09989732  
 ; Patent No. US20020123463A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavini, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730PIC57

; CURRENT APPLICATION NUMBER: US/09/989,732

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

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; PRIOR FILING DATE: 1997-11-13

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; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
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Best Local Similarity 100.0%; Pred. No. 7.5e-47;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-991-073-408
Sequence 408, Application US/09991073
Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2730P1C15
CURRENT APPLICATION NUMBER: US/09/991.073
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
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; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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RESULT 9  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Napier, Mary A.  
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; APPLICANT: Williams, P. Mickey  
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Query Match 100.0%; Score 502; DS 9; Length 104;  
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65 PRIOR FILING DATE: 1998-07-07  
66 PRIOR APPLICATION NUMBER: 60/092182  
67 PRIOR FILING DATE: 1998-07-09

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RESULT 10

US-09-993-604-408  
; Sequence 408, Application US/09993604  
; Patent No. US20020137075A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Iuc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P27301C25  
; CURRENT APPLICATION NUMBER: US/09/993,604  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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; Patent No. US20020137890A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C22  
; CURRENT APPLICATION NUMBER: US/09/990,456  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
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Query Match 100.0%; Score 502; DB 9; Length 104;  
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Query Match 100.0%; Score 502; DB 9; Length 104;  
 Best local similarity 100.0%; Pred. No. 7.5e-47;  
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKLAALIGLCVALSCSSAAAFIVGSAKPVAOPVAALSAEAGAGTIANPLGTINPKLL	60
Db	1	MKLAALIGLCVALSCSSAAAFIVGSAKPVAOPVAALSAEAGAGTIANPLGTINPKLL	60
Qy	61	LSSIGIPVNHLEIGSQKCVAEELGQAVGAVKALKALGALTVEG	104
Db	61	LSSIGIPVNHLEIGSQKCVAEELGQAVGAVKALKALGALTVEG	104

RESULT 12

US-09-989-721-408  
 ; Sequence 408, Application US/09989721  
 ; Patent No. US20020142961A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary B.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2730P1C55  
 ; CURRENT APPLICATION NUMBER: US/09/989,721  
 ; CURRENT FILING DATE: 2001-11-19  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065186  
 ; PRIOR FILING DATE: 1997-11-12  
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 ; PRIOR FILING DATE: 1997-11-13  
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 ; PRIOR FILING DATE: 1997-11-24  
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 ; PRIOR FILING DATE: 1998-02-25  
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; PRIOR FILING DATE: 1998-06-04  
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 ; PRIOR APPLICATION NUMBER: 60/088167  
 ; PRIOR FILING DATE: 1998-06-05  
 ; PRIOR APPLICATION NUMBER: 60/088202  
 ; PRIOR FILING DATE: 1998-06-05  
 ; PRIOR APPLICATION NUMBER: 60/088212  
 ; PRIOR FILING DATE: 1998-06-05  
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;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 502; DB 9; Length 104;  
Best Local Similarity 100.0%; Pred. No. 7.5e-47;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MKLAALGLCVALLSCSSAAFLVGSAPVQVPAALLESAAEAGAGTLANPLGTLNPKLL 60  
Db 1 MKLAALGLCVALLSCSSAAFLVGSAPVQVPAALLESAAEAGAGTLANPLGTLNPKLL 60  
  
Qy 61 LSSIGIPVNHLEGSQKCVAEELGPQAVGAVKALKALIGALTVEG 104  
Db 61 LSSIGIPVNHLEGSQKCVAEELGPQAVGAVKALKALIGALTVEG 104

RESULT 13

US-09-992-598-408  
; Sequence 408, Application US/09992598  
; Patent No. US20020160384A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavins, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730FIC20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
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; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
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; PRIOR FILING DATE: 1998-06-02  
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; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087759  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087827  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: 60/088021  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088025  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088026  
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; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088029  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088030  
; PRIOR FILING DATE: 1998-06-04

RESULT 14  
US-09-989-293A-408  
; Sequence 408, Application US/09989293A  
; Patent No. US20020177164A1

GENERAL INFORMATION:	1	PRIOR FILING DATE: 1998-06-04	2
APPLICANT: Ashkenazi, Avi J.	2	PRIOR APPLICATION NUMBER: 60/088167	3
APPLICANT: Baker, Kevin P.	3	PRIOR FILING DATE: 1998-06-05	4
APPLICANT: Botstein, David	4	PRIOR APPLICATION NUMBER: 60/088202	5
APPLICANT: Desnoyers, Luc	5	PRIOR FILING DATE: 1998-06-05	6
APPLICANT: Eaton, Dan L.	6	PRIOR APPLICATION NUMBER: 60/088212	7
APPLICANT: Ferrara, Napoleone	7	PRIOR FILING DATE: 1998-06-05	8
APPLICANT: Fong, Sherman	8	PRIOR APPLICATION NUMBER: 60/088217	9
APPLICANT: Gerber, Hanspeter	9	PRIOR FILING DATE: 1998-06-05	10
APPLICANT: Gerritsen, Mary E.	10	PRIOR APPLICATION NUMBER: 60/088655	11
APPLICANT: Goddard, Audrey	11	PRIOR FILING DATE: 1998-06-09	12
APPLICANT: Godowski, Paul J.	12	PRIOR APPLICATION NUMBER: 60/088734	13
APPLICANT: Grimaldi, J. Christopher	13	PRIOR FILING DATE: 1998-06-10	14
APPLICANT: Gurney, Austin L.	14	PRIOR APPLICATION NUMBER: 60/088738	15
APPLICANT: Kijavini, Ivar J.	15	PRIOR FILING DATE: 1998-06-10	16
APPLICANT: Napier, Mary A.	16	PRIOR APPLICATION NUMBER: 60/088742	17
APPLICANT: Pan, James	17	PRIOR FILING DATE: 1998-06-10	18
APPLICANT: Paoni, Nicholas F.	18	PRIOR APPLICATION NUMBER: 60/088810	19
APPLICANT: Roy, Margaret Ann	19	PRIOR FILING DATE: 1998-06-10	20
APPLICANT: Stewart, Timothy A.	20	PRIOR APPLICATION NUMBER: 60/088824	21
APPLICANT: Tumas, Daniel	21	PRIOR FILING DATE: 1998-06-10	22
APPLICANT: Watanabe, Colin K.	22	PRIOR APPLICATION NUMBER: 60/088826	23
APPLICANT: Williams, P. Mickey	23	PRIOR FILING DATE: 1998-06-10	24
APPLICANT: Wood, William I.	24	PRIOR APPLICATION NUMBER: 60/088858	25
APPLICANT: Zhang, Zemin	25	PRIOR FILING DATE: 1998-06-11	26
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	26	PRIOR APPLICATION NUMBER: 60/088861	27
TITLE OF INVENTION: Acids Encoding the Same	27	PRIOR FILING DATE: 1998-06-11	28
FILE REFERENCE: P2730PlC66	28	PRIOR APPLICATION NUMBER: 60/088876	29
CURRENT APPLICATION NUMBER: US/09/989, 293A	29	PRIOR FILING DATE: 1998-06-11	30
CURRENT FILING DATE: 2001-11-20	30	PRIOR APPLICATION NUMBER: 60/089105	31
PRIOR APPLICATION NUMBER: 60/049787	31	PRIOR FILING DATE: 1998-06-12	32
PRIOR FILING DATE: 1997-06-16	32	PRIOR APPLICATION NUMBER: 60/089440	33
PRIOR APPLICATION NUMBER: 60/062250	33	PRIOR FILING DATE: 1998-06-16	34
PRIOR FILING DATE: 1997-10-17	34	PRIOR APPLICATION NUMBER: 60/089512	35
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PRIOR FILING DATE: 1997-11-13	38	PRIOR APPLICATION NUMBER: 60/089532	39
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PRIOR FILING DATE: 1997-11-24	40	PRIOR APPLICATION NUMBER: 60/089538	41
PRIOR APPLICATION NUMBER: 60/075945	41	PRIOR FILING DATE: 1998-06-17	42
PRIOR FILING DATE: 1998-02-25	42	PRIOR APPLICATION NUMBER: 60/089598	43
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PRIOR FILING DATE: 1998-06-02	54	PRIOR APPLICATION NUMBER: 60/089908	55
PRIOR APPLICATION NUMBER: 60/087759	55	PRIOR FILING DATE: 1998-06-18	56
PRIOR FILING DATE: 1998-06-02	56	PRIOR APPLICATION NUMBER: 60/089947	57
PRIOR APPLICATION NUMBER: 60/087827	57	PRIOR FILING DATE: 1998-06-19	58
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PRIOR FILING DATE: 1998-06-04	66	PRIOR APPLICATION NUMBER: 60/090254	67
PRIOR APPLICATION NUMBER: 60/088029	67	PRIOR FILING DATE: 1998-06-22	68
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PRIOR FILING DATE: 1998-06-04	72	PRIOR APPLICATION NUMBER:	

APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC61  
CURRENT APPLICATION NUMBER: US/09/989,735  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05

APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
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APPLICANT: Ferrara, Napoleone  
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APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC61  
CURRENT APPLICATION NUMBER: US/09/989,735  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05

Query Match 100.0%; Score 502; DB 9; Length 104;  
Best Local Similarity 100.0%; Pred. No. 7.5e-47;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLAALLGLCVALLSCSSAAAFVGSAPVQVVALESAAEAGAGTLANPLGTLNPLKLL 60  
QY 61 LSSLGIPVNHLEGGSKVVAELGPOAVGAVKALKALLGALTVFG 104  
DB 61 LSSLGIPVNHLEGGSKVVAELGPOAVGAVKALKALLGALTVFG 104

RESULT 15  
US-09-989-735-408  
; Sequence 408, Application US/09989735  
; Publication No. US20020193299A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:16:40 ; Search time 7.24797 Seconds  
(without alignments)  
740.773 Million cell updates/sec

Title: US-09-700-770-9  
Perfect score: 502  
Sequence: 1 MKLAALLGLCVALLSCSSAAA.....QAVGAVKALKALLGALTVFG 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	160	31.9	93	2	US-08-964-725-14
2	83	16.5	673	3	US-09-196-387-8
3	83	16.5	673	4	US-09-841-835-8
4	83	16.5	949	3	US-09-196-387-10
5	83	16.5	949	4	US-09-841-835-10
6	83	16.5	1327	3	US-09-196-387-2
7	83	16.5	1327	4	US-09-841-835-2
8	83	16.5	1327	4	US-09-972-115A-8
9	82.5	16.4	718	4	US-09-252-991A-25696
10	78.5	15.6	255	4	US-09-252-991A-21756
11	77	15.3	540	4	US-09-252-991A-29143
12	73.5	14.6	443	3	US-09-088-425-2
13	73.5	14.6	447	4	US-09-639-378A-2
14	73.5	14.6	776	4	US-09-523-849-34
15	72	14.3	236	1	US-08-452-531-3
16	72	14.3	236	2	US-08-460-746A-3
17	72	14.3	236	2	US-08-460-555-3
18	72	14.3	236	3	US-08-460-666-3
19	69.5	13.8	423	4	US-09-073-009-142
20	69.5	13.8	423	4	US-09-073-010-142
21	69.5	13.8	710	4	US-09-287-849-16
22	69.5	13.8	856	4	US-09-287-849-12
23	69	13.7	468	4	US-09-252-991A-28114
24	68.5	13.6	163	1	US-08-252-991A-22281
25	68	13.5	461	1	US-08-194-338-4
26	68	13.5	480	4	US-09-543-681A-4680
27	67	13.3	419	4	US-09-252-991A-26821

28	66.5	13.2	323	4	US-09-489-039A-13907	Sequence 13907, A
29	66	13.1	310	4	US-09-489-039A-12597	Sequence 12597, A
30	66	13.1	390	4	US-09-647-224A-2	Sequence 2, Appli
31	66	13.1	587	4	US-09-252-991A-31479	Sequence 31479, A
32	66	13.1	638	2	US-08-426-125-4	Sequence 4, Appli
33	66	13.1	638	2	US-08-455-355-4	Sequence 4, Appli
34	66	13.1	638	4	US-09-367-512-3	Sequence 3, Appli
35	66	13.1	1043	4	US-08-851-567B-61	Sequence 61, Appl
36	65.5	13.0	346	4	US-09-134-000C-4469	Sequence 4469, Ap
37	65.5	13.0	407	4	US-09-489-039A-10855	Sequence 10855, A
38	65.5	13.0	593	2	US-08-591-079-10	Sequence 8, Appli
39	65.5	13.0	593	2	US-08-591-079-10	Sequence 10, Appli
40	65.5	13.0	645	4	US-09-543-681A-6140	Sequence 6140, Ap
41	65.5	13.0	4928	3	US-09-036-987A-5	Sequence 5, Appli
42	65.5	13.0	4928	3	US-09-370-700-5	Sequence 5, Appli
43	65.5	13.0	4928	4	US-09-603-207-5	Sequence 5, Appli
44	65	12.9	180	4	US-09-489-039A-12312	Sequence 12312, A
45	65	12.9	269	4	US-09-107-532A-5682	Sequence 5682, Ap

## ALIGNMENTS

RESULT 1  
US-08-964-725-14  
; Sequence 14, Application US/08964725  
; Patent No. 5939265  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, Maurice  
; APPLICANT: FRIEDMAN, Paula N.  
; APPLICANT: GORDON, Julian C.  
; APPLICANT: HODGES, Steven C.  
; APPLICANT: KLASS, Michael R.  
; APPLICANT: KRATOCHVIL, Jon D.  
; APPLICANT: ROBERTS-RAPP, Lisa  
; APPLICANT: RUSSELL, John C.  
; APPLICANT: STROUPE, Steven D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; FOR DETECTING DISEASES OF THE LUNG  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/964,725  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 5997.US.PI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 93 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear



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MOLECULE TYPE: No. 5939265e
US-08-964-725-14

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Matches 44; Conservative 9; Mismatches 38; Indels 10; Gaps 2;

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QY 60 LLSLGLIPVNHLEGSQKVAELGPGQAVGAVKALKALGAL 100
Db 52 LKTLGISVEHLVEGURKCVNELGPEASEAVKLLLEALSHL 92

RESULT 2
US-09-196-387-8
; Sequence 8, Application US/09196387
; Patent No. 6277613
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,387
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-196-387-8

Query Match
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Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

QY 15 CSSAAAFVLSAKPVAQVVALESAA-----EAGAGTLANPLGTLNPLKLLSSLGIPVN 69
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QY 70 HLIEGSQ-----KCVAEIGPGQAVGAVKALKALGAL 100
Db 149 SLAESPEAAGVSTAPLPGGAAGPGTGVPAVSGAL 183

RESULT 3
US-09-196-387-10
; Sequence 10, Application US/09196387
; Patent No. 6277613
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841,835
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-841-835-8

Query Match
Best Local Similarity 30.5%; Score 83; DB 4; Length 673;
Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

QY 15 CSSAAAFVLSAKPVAQVVALESAA-----EAGAGTLANPLGTLNPLKLLSSLGIPVN 69
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QY 70 HLIEGSQ-----KCVAEIGPGQAVGAVKALKALGAL 100
Db 149 SLAESPEAAGVSTAPLPGGAAGPGTGVPAVSGAL 183

RESULT 4
US-09-196-387-10
; Sequence 10, Application US/09196387
; Patent No. 6277613
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,387
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,225
; FILING DATE: June 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-196-387-8

Query Match
Best Local Similarity 30.5%; Score 83; DB 3; Length 673;
Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

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QY 70 HLIEGSQ-----KCVAEIGPGQAVGAVKALKALGAL 100
Db 149 SLAESPEAAGVSTAPLPGGAAGPGTGVPAVSGAL 183
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RESULT 3
US-09-841-835-8
; Sequence 8, Application US/09841835
; Patent No. 6506587
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841,835
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-841-835-8

Query Match
Best Local Similarity 30.5%; Score 83; DB 4; Length 673;
Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

QY 15 CSSAAAFVLSAKPVAQVVALESAA-----EAGAGTLANPLGTLNPLKLLSSLGIPVN 69
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QY 70 HLIEGSQ-----KCVAEIGPGQAVGAVKALKALGAL 100
Db 149 SLAESPEAAGVSTAPLPGGAAGPGTGVPAVSGAL 183

RESULT 4
US-09-196-387-10
; Sequence 10, Application US/09196387
; Patent No. 6277613
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-841-835-8

Query Match
Best Local Similarity 30.5%; Score 83; DB 4; Length 673;
Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

QY 15 CSSAAAFVLSAKPVAQVVALESAA-----EAGAGTLANPLGTLNPLKLLSSLGIPVN 69
Db 90 CSTTCTICVAAAPVV-PAVSTSSAAGVAPNPGSGNNSPSSSSPTSSSSSPSPSGS 148

QY 70 HLIEGSQ-----KCVAEIGPGQAVGAVKALKALGAL 100
Db 149 SLAESPEAAGVSTAPLPGGAAGPGTGVPAVSGAL 183

RESULT 4
US-09-196-387-10
; Sequence 10, Application US/09196387
; Patent No. 6277613
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-841-835-8

Query Match
Best Local Similarity 30.5%; Score 83; DB 4; Length 673;
Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

QY 15 CSSAAAFVLSAKPVAQVVALESAA-----EAGAGTLANPLGTLNPLKLLSSLGIPVN 69
Db 90 CSTTCTICVAAAPVV-PAVSTSSAAGVAPNPGSGNNSPSSSSPTSSSSSPSPSGS 148

QY 70 HLIEGSQ-----KCVAEIGPGQAVGAVKALKALGAL 100
Db 149 SLAESPEAAGVSTAPLPGGAAGPGTGVPAVSGAL 183
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; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/09/196,387
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,225
; FILING DATE: June 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 949 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-841-835-10

Query Match 16.5%; Score 83; DB 3; Length 949;
Best Local Similarity 30.5%; Pred. No. 0.45;
Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

QY 15 CSSAAFLVGSXKPVQAPVAALSA-----EAGAGTLANPLGLNPKLLSSLGIPVN 69
Db 90 CSTTSTICTVAAPVV-PAVSTSSAAGVAPNPAGSGNNSSPTSSSSSSPSSPGS 148

QY 70 HLIQSQ-----KCVAEIQLPQAVGAVKALKAL 100
Db 149 SLAESPEAAGVSTAPLPGAGPGTGVPVAVSGAL 183

RESULT 5
US-09-841-835-10
; Sequence 10, Application US/09841835
; Patent No. 6506587
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841,835
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:

; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/09/196,387
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,225
; FILING DATE: June 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 949 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-841-835-10

Query Match 16.5%; Score 83; DB 4; Length 949;
Best Local Similarity 30.5%; Pred. No. 0.45;
Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

QY 15 CSSAAFLVGSXKPVQAPVAALSA-----EAGAGTLANPLGLNPKLLSSLGIPVN 69
Db 90 CSTTSTICTVAAPVV-PAVSTSSAAGVAPNPAGSGNNSSPTSSSSSSPSSPGS 148

QY 70 HLIQSQ-----KCVAEIQLPQAVGAVKALKAL 100
Db 149 SLAESPEAAGVSTAPLPGAGPGTGVPVAVSGAL 183

RESULT 6
US-09-196-387-2
; Sequence 2, Application US/09196387
; Patent No. 6277613
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,387
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,225
; FILING DATE: June 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1327 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

```
Query Match      16.5%; Score 83; DB 4; Length 1327;
Best Local Similarity 30.5%; Pred.No. 0.71;
Matches          29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

Qy    15 CSSAAFLVGSAKPVAQPVAALESAA-----EAGAGTLANPLGTINPLKLLISSLGIPVN 69
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db     90 CSITTICTVAAPVV-PAVSTSSAAGVAPNPAGSGSNNSPTSSSSSPSSPSGSS 148
       ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

Qy    70 HLEIGSQ----KCVAEIQQPVAVKALKLIGAL 100
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
```

	Query Match	16.4%;	Score 82.5;	DB 4;	Length 718;	
	Best Local Similarity Matches	37.3%;	Fred. No. 0.35;			
	Matches	25;	Conservative	8;	Mismatches 31;	Indels 3; Gaps 2;
Qy	24	GSAPVPAOPVAALBSAAEA--GAGTLANPLGTLPKILLSGLGPVNNHLIEGSKQCVAE	81	:	:	:
		:	:	:	:	:
Dd	139	GGALLAGLPPAFAFQLAQVVFDAGELRYVLGIQQARIVGAALG-DVEHLYVEGEDAQADE	197	:	:	:
Qy	82	LGFQAQVG	88	:	:	:

Db 198 AGPGALG 204

RESULT 10

US-09-252-991A-21756

Sequence 21756, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21756

LENGTH: 255

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21756

Query Match 15.6%; Score 78.5; DB 4; Length 255;

Best Local Similarity 24.1%; Pred. No. 0.25; Mismatches 10; Indels 71; Gaps 6;

Matches 39; Conservative 10;

Db 10 CVALSCSSA--AAFLVGSAPVPAQVAALGSAAGA-----GTLANPLGTLNPLK 58

7 CLAAECCAAHPAFCGRPGVRRAGEAFPSAVEAGVQADLRVEHLGYRATGLGLVGD-- 64

59 LLLSLGHPVNH-----LLEG-----74

65 -LLEGRLVRPHARPEHQVHSGDGTGVLVGGDLGAGLDTFGGQAGLAEHHRQHAEEA 123

75 -----SOKVAELGPOAVGAV--KALKALLGALTVF 103

124 GVGADQLFRVSGRCALENGIEAIGVVLERRAFAFGKGLAVF 165

RESULT 11

US-09-252-991A-29143

Sequence 29143, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29143

LENGTH: 540

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29143

Query Match 15.3%; Score 77; DB 4; Length 540;

Best Local Similarity 30.0%; Pred. No. 1.1;

Matches 33; Conservative 13; Mismatches 40; Indels 24; Gaps 5;

Db 4 AALLGLCVLSCSSA-----AAFLVGSAPVPAQVAALGSAAGA-----AEAGAGTL 47

302 AQVLGNLVGSCAGCAQCMVAISAAVFGAARWIPELAAERMAALRPGHWQDDPAAYGPL 361

48 ANPLGTLNPLKLLSLGHPVNHIEGSKCVAE-----LGPQAVGAV 90

Db 362 ISPQARQVRLRLIAEKAEGAECLLDGSQ-CQVEGYPNGNWLGTTLFRAV 410

RESULT 12

US-09-088-425-2

Sequence 2, Application US/09088425

Patent No. 6171843

GENERAL INFORMATION:

APPLICANT: BANDMAN, OLGA

APPLICANT: LAL, PREETI

APPLICANT: CORLEY, NEIL C.

APPLICANT: PATTERSON, CHANDRA

APPLICANT: BAUGHN, MARIAH R.

TITLE OF INVENTION: HUMAN ISOMERASE-LIKE PROTEINS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/088,425

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0529 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 443 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: TMLR3DT01

CLONE: 289973

US-09-088-425-2

Query Match 14.6%; Score 73.5; DB 3; Length 443;

Best Local Similarity 34.1%; Pred. No. 2.1;

Matches 29; Conservative 9; Mismatches 26; Indels 21; Gaps 4;

QY 35 ALESAEAGAGTLANPLGTLNPLK-----LLLS-----LGPVNHIEGSKCV 79

326 ALFEALEQG-----QSLGFVEFLDGPAGVLECLVSSGMLVPELAIPVYLL-GALTWL 379

Db 80 ABLGPQAVGAVKALKALLGALTTFVG 104

380 SETRAQAAGGGAGVAELLGPLELVG 404

RESULT 13

US-09-639-378A-2

Sequence 2, Application US/09639378A

Patent No. 6524838

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

```

; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil. C.
; APPLICANT: Patterson, Chandra
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN PEPTIDYL-PROLYL ISOMERASES
; FILE REFERENCE: PF-0529-1 DIV
; CURRENT APPLICATION NUMBER: US/09/639,378A
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 09/088,425
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6524838 289973CD1
US-09-639-378A-2

Query Match 14.6%; Score 73.5; DB 4; Length 447;
Best Local Similarity 34.1%; Pred. No. 2.1;
Matches 29; Conservative 26; Mismatches 26; Indels 21; Gaps 4;

QY 35 ALESAEAGAGTLANPLGTINPLK-----LLLS-----LGIPVNHIEGSKCV 79
Db 328 ALEEALEQ-----QSLGVEPLDGPAGAVLECLVLSGMLVPELAIPVYLL-GALTML 381

QY 80 AELGPOAVGAVKALKALGALTFFG 104
Db 382 SETRAQAAGGAGVLELGLPLNG 406

RESULT 14
US-09-849-34
; Sequence 34, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnaghi, Paola
; APPLICANT: Bosotti, Roberta
; APPLICANT: Scacheri, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523,849
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 34
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank Accession No. 6458561 g5672676
US-09-523-849-34

Query Match 14.6%; Score 73.5; DB 4; Length 776;
Best Local Similarity 33.7%; Pred. No. 4.5;
Matches 28; Conservative 11; Mismatches 31; Indels 13; Gaps 4;

QY 10 CVALSCSAAAFVGSAPVQPVAALESAAEAGAGTLANP--LGTNPLKLLSSLGIP 67
Db 490 CIIVSSSAVSPSECTSSDSCLPFSASBPAGLGG-LATPGLLTSSPVLASPFLL--- 545

QY 68 VNHIEGSKCVAEILGPOA-VGA 89
Db 546 -----GQSATPVLQSQAGLGA 562
```

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RESULT 15
US-08-452-531-3
; Sequence 3, Application US/08452531
; Patent No. 5733778
; GENERAL INFORMATION:
; APPLICANT: MATLASHEWSKI, Gregory
; APPLICANT: CHAREST, Hugues
; TITLE OF INVENTION: GENES OF LEISHMANIA WHICH ARE DIFFERENTIALLY-
; TITLE OF INVENTION: EXPRESSED IN AMASTIGOTE FORM
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,531
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/115,987
; FILING DATE: 03-SEP-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-448 MIS:bh
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-452-531-3

Query Match 14.3%; Score 72; DB 1; Length 236;
Best Local Similarity 29.8%; Pred. No. 1.3;
Matches 31; Conservative 15; Mismatches 42; Indels 16; Gaps 4;

QY 1 MKLAALLGLCVALSCSSAAAFVGSAP--VQPVAALESAAEAGAGTLANPLGTINPLK 58
Db 1 MKIRSVRPLVLLVCVAAVLALSASAEHPKAAVDVGFL-SVGFPQSVGVLSPVQAVGPLS 59

QY 59 LLLSSLGIPVNHIEGSKCVAEILGPOAVGAVKALKALGALTV 102
Db 60 VGPQSVG-PLS-----VGPOAVGPLSVGPQSVGPLSV 90

Search completed: June 2, 2004, 20:23:17
Job time : 8.24797 secs
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2004, 19:59:24 ; Search time 24.778 Seconds

Title: US-09-700-770-9

Perfect score: 502

Sequence: 1 MKLAALLGLCVLSCSSAAA.....QAVGAVKALKALGALTVEG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502	100.0	104	3	Aay66757 Membrane-
2	502	100.0	104	3	Aay44458 Human lun
3	502	100.0	104	3	Aay87288 Human sig
4	502	100.0	104	4	Aab65280 Human PRO
5	502	100.0	104	5	Aau86141 Human PRO
6	502	100.0	104	6	Abu58095 Human PRO
7	502	100.0	104	6	Abu59173 Novel hum
8	502	100.0	104	6	Abu82685 Human sec
9	502	100.0	104	6	Aao19895 Human ute
10	502	100.0	104	6	Abu60604 Human sec
11	502	100.0	104	6	Abu13986 Human PRO
12	502	100.0	104	6	Abu72571 Novel hum
13	502	100.0	104	6	Abu59320 Human sec
14	502	100.0	104	6	Abu26017 Human PRO
15	502	100.0	104	6	Abu59026 Human sec
16	502	100.0	104	6	Abu92404 Novel hum
17	502	100.0	104	6	Abu59469 Novel hum
18	502	100.0	104	6	Abu92235 Novel hum
19	502	100.0	104	6	Abu10941 Human PRO
20	502	100.0	104	6	Abu81693 Novel hum
21	502	100.0	104	6	Abu88632 Human sec
22	502	100.0	104	6	Abu34146 Human PRO
23	502	100.0	104	6	Ada37919 Human sec
24	502	100.0	104	6	Ada21605 Human sec
25	502	100.0	104	6	Ada10392 Human sec

26	502	100.0	104	6	ADA17936	Ada17936 Human PRO
27	502	100.0	104	6	ADA28044	Ada28044 Human sec
28	502	100.0	104	6	ADA94624	Ada94624 Human sec
29	502	100.0	104	6	ADA38849	Ada38849 Human sec
30	502	100.0	104	6	ADA92970	Ada92970 Human sec
31	502	100.0	104	7	ABO53232	Abu53232 Human sec
32	502	100.0	104	7	ADA22531	Ada22531 Human sec
33	502	100.0	104	7	ABO22602	Abu22602 Human sec
34	502	100.0	104	7	ADA06697	Ada06697 Human sec
35	502	100.0	104	7	ADA39390	Ada39390 Human sec
36	502	100.0	104	7	ADB96416	Adb96416 Human PRO
37	502	100.0	104	7	ADC57888	Adc57888 Human PRO
38	502	100.0	104	7	ADC55252	Adc55252 Human PRO
39	502	100.0	104	7	ADC12119	Adc12119 Human PRO
40	502	100.0	104	7	ADC56541	Adc56541 Human PRO
41	502	100.0	104	7	ADC07596	Adc07596 Human sec
42	502	100.0	104	7	ADC11586	Adc11586 Human sec
43	502	100.0	104	7	ADC14708	Adc14708 Novel hum
44	502	100.0	104	7	ADD08240	Add08240 Novel hum
45	502	100.0	104	7	ADC82065	Adc82065 Human PRO

## ALIGNMENTS

RESULT 1  
AAY66757  
ID AAY66757 standard; protein; 104 AA.  
XX  
AC AAY66757;  
XX  
DT 05-FPR-2000 (first entry)  
XX  
DB Membrane-bound protein PRO1245.  
XX  
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.  
XX  
OS Homo sapiens.  
XX  
PN W09963088-A2.  
XX  
PD 09-DEC-1999.  
XX  
PF 02-JUN-1999; 99WO-US012252.  
XX  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 03-JUN-1998; 98US-0087759P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088722P.  
PR 10-JUN-1998; 98US-0088730P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088740P.  
PR 10-JUN-1998; 98US-0088741P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088811P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088825P.

10

QY 61 LSSLGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTVEG 104  
DB 61 LSSLGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTVEG 104

RESULT 2  
AAAY44458  
ID AAY44458 standard; protein; 104 AA.

XX AC AAY44458;  
XX DT 27-MAR-2000 (first entry)  
XX DE Human lung specific gene protein Lng107.  
XX KW Lung Specific Gene; LSG; Lng107; human; diagnostic marker; prognosticate;  
XX KW lung cancer; diagnosis.  
XX OS Homo sapiens.  
XX EN WO960160-AL.  
XX PD 25-NOV-1999.  
XX PF 12-MAY-1999; 99WO-US010344.  
XX PR 21-MAY-1998; 98US-0086212P.  
XX PA (DIAD-) DIADEXUS LLC.  
XX PI Yang F, Macina RA, Sun Y;  
XX WPI; 2000-116320/10.  
XX DR N-PSDB; AAZ29723.  
XX PT A new method for diagnosing, monitoring and staging lung cancer.  
XX PS Example 2; Page 38-39; 40pp; English.

CC The present sequence is a lung specific gene (LSG) protein Lng107 from  
CC human clone ID 586271. The LSG has high level of tissue specificity for  
CC lungs and is overexpressed in cancerous tissues. The sequence serves as a  
CC diagnostic marker for detecting, monitoring, staging and prognosticating  
CC lung cancer. The diagnosis involves comparing levels of LSG in samples  
CC obtained from patient and normal control  
XX Sequence 104 AA;  
QY Query Match 100.0%; Score 502; DB 3; Length 104;  
DB Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLAALLGLCVLSCSSAAAFVLSAKPVAQPVAALSAEAGAGTLANPLGTLNPKLL 60  
DB 1 MKLAALLGLCVLSCSSAAAFVLSAKPVAQPVAALSAEAGAGTLANPLGTLNPKLL 60  
QY 61 LSSLGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTVEG 104  
DB 61 LSSLGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTVEG 104

RESULT 3  
AAAY87288  
ID AAY87288 standard; protein; 104 AA.  
XX AC AAY87288;  
XX DT 11-MAY-2000 (first entry)  
XX DE Human signal peptide containing protein HSPP-65 SEQ ID NO:65.  
XX KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;

inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
antimicrobial; neuroprotective; cardiovascular; hepatotropic;  
antischismatic; gene therapy; cell proliferation; neurological disorder;  
reproductive disorder; developmental disorder; arteriosclerosis;  
cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
Parkinson's disease; Huntington's disease; ovulatory defect;  
muscular dystrophy.

OS Homo sapiens.  
XX WO200000610-A2.  
XX PD 06-JAN-2000.  
XX PF 25-JUN-1999; 99WO-US014484.  
XX PR 26-JUN-1998; 98US-0090762P.  
XX PR 31-JUL-1998; 98US-0094983P.  
XX PR 01-OCT-1998; 98US-0102686P.  
XX PR 11-DEC-1998; 98US-0112129P.  
XX (INCY-) INCYTE PHARM INC.  
XX Ial P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn ME;  
XX PI Akertlom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
XX PI Bandman O;  
XX WPI; 2000-160673/14.  
XX DR N-PSDB; AAZ98173.

New human signal peptide-containing proteins useful in treatment,  
prevention and diagnosis of e.g. cancer, inflammation and cardiovascular  
disease.

Claim 1; Page 206; 327pp; English.

AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the  
human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have  
anticancer, anti-inflammatory, antimicrobial, neuroprotective, hepatotropic,  
neuroprotective, cardiovascular and antiasthmatic activities, and can be  
used in gene therapy. HSPPs can be used to treat or prevent disorders  
associated with decreased activity or function of HSPP. Antagonists of  
HSPP are used to treat or prevent disorders associated with increased  
activity or function of HSPP. Such diseases include cell proliferation  
(including cancer), inflammation, cardiovascular, neurological,  
reproductive or developmental disorders, (e.g. arteriosclerosis,  
cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
asthma, Crohn's disease, microbial or other infections, congestive or  
ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP  
nucleic acids can be used for the recombinant production of HSPP, for  
detecting HSPP in standard hybridisation and amplification assays (for  
diagnosis and monitoring), in gene therapy, as antisense, triplex-forming  
or ribozyme therapeutics, for detecting related sequences or genetic  
variations, and for chromosomal mapping. HSPP are also used to raise  
specific antibodies (Ab) and to screen for agonists and antagonists  
(potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP  
-related diseases (in usual immunoassays), as therapeutic antagonists, in  
competitive drug screens, and for purification of HSPP from natural  
sources

Sequence 104 AA;

Query Match 100.0%; Score 502; DB 3; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAALLGLCVLSCSSAAAFVLSAKPVAQPVAALSAEAGAGTLANPLGTLNPKLL 60  
DB 1 MKLAALLGLCVLSCSSAAAFVLSAKPVAQPVAALSAEAGAGTLANPLGTLNPKLL 60  
QY 61 LSSLGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTVEG 104



chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

Query Match 100.0%; Score 502; DB 4; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48; Indels 0; Gaps 0;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLAALLGLCVLSCSSAAAFVGSAPVQAPVAALESAAEAGAGTLANPLGTLNPKLL 60  
DB 1 MKLAALLGLCVLSCSSAAAFVGSAPVQAPVAALESAAEAGAGTLANPLGTLNPKLL 60  
QY 61 LSSLGIPVNHLEGSQKCVAEFGPQAVGAVKALKALGALTVEG 104  
DB 61 LSSLGIPVNHLEGSQKCVAEFGPQAVGAVKALKALGALTVEG 104

RESULT 5  
AAU86141  
ID AAU86141 standard; protein; 104 AA.  
XX AC AAU86141;  
XX DT 15-JUL-2002 (first entry)  
XX DE Human PRO1245 polypeptide.

Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoele disorder; inflammatory disorder; immune disorder; angiogenic disorder; cytostatic; neuroprotective.

Homo sapiens.  
WO20153486-A1.  
26-JUL-2001.  
11-FEB-2000; 2000WO-US003565.

08-VAR-1999; 99WO-US005028.  
11-MAR-1999; 99US-0123972P.  
11-MAY-1999; 99US-0133459P.  
02-JUN-1999; 99WO-US012252.  
22-JUN-1999; 99US-0140653P.  
20-JUL-1999; 99US-0144758P.  
26-JUL-1999; 99US-0145698P.  
28-JUL-1999; 99US-0146222P.  
17-AUG-1999; 99US-0149395P.  
31-AUG-1999; 99US-0151689P.  
01-SEP-1999; 99WO-US020111.  
15-SEP-1999; 99WO-US021090.  
30-NOV-1999; 99WO-US028313.  
01-DEC-1999; 99WO-US028301.  
01-DEC-1999; 99WO-US028634.  
05-JAN-2000; 2000WO-US000219.

(GETH ) GENENTECH INC.  
Ashkenazi AJ, Goddard A, Godowski RJ, Gurney AL, Hillan KJ;  
Marsters SA, Pitti RM, Roy MA, Smith V, Stone DM;  
Watanabe CK, Wood WI;  
WF.; 2002-205567/26.

61 LSSLGIPVNHLEGSQKCVAEFGPQAVGAVKALKALGALTVEG 104

RESULT 4  
AAB65280  
ID AAB65280 standard; protein; 104 AA.  
XX AC AAB65280;  
XX DT 02-APR-2001 (first entry)  
XX DE Human PRO1245 (UNQ629) protein sequence SEQ ID NO:408.  
XX KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;  
XX KW cancer; chromosomal mapping; gene mapping; tissue typing;  
XX KW diagnostic assay.

OS Homo sapiens.  
XX PN WO200073454-A1.  
XX PD 07-DEC-2000.  
XX PF 30-MAR-2000; 2000WO-US008439.

02-JUN-1999; 99WO-US012252.  
23-JUN-1999; 99US-0141037P.  
07-JUL-1999; 99US-0143048P.  
20-JUL-1999; 99US-0144758P.  
26-JUL-1999; 99US-0145698P.  
28-JUL-1999; 99US-0146222P.  
17-AUG-1999; 99US-0149395P.  
15-SEP-1999; 99WO-US021090.  
08-OCT-1999; 99US-0158663P.  
30-NOV-1999; 99WO-US028313.  
01-DEC-1999; 99WO-US028301.  
16-DEC-1999; 99WO-US030095.  
20-DEC-1999; 99WO-US030911.  
05-JAN-2000; 2000WO-US000219.  
11-FEB-2000; 2000WO-US003376.  
18-FEB-2000; 2000WO-US004341.  
22-FEB-2000; 2000WO-US004414.  
24-FEB-2000; 2000WO-US004914.  
02-MAR-2000; 2000WO-US005841.  
15-MAR-2000; 2000WO-US006884.  
20-MAR-2000; 2000WO-US007377.

(GETH ) GENENTECH INC.  
Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;  
Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI;  
Zhang Z;

WPI; 2001-032160/04.  
N-PSDB; AAF44249.

PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.

Claim 12; Fig 290; 935pp; English.  
The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in

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DR N-PSDB; ABK40267.
XX
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.
XX
XX Claim 61; Fig 28; 302pp; English.
PS
PS
XX The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The PRO
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
CC treating benign or malignant tumors (e.g. renal, kidney, bladder,
CC breast, etc), leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytic, hypothalamic, glandular, macrophagal,
CC stromal and blastocoeleic disorders, inflammatory, immune and angiogenic
CC disorders. The polynucleotide sequences are also useful in gene therapy.
CC AAU86128-AAU86162 represent the human PRO polypeptides of the invention.
XX
XX
SQ Sequence 104 AA;
Query Match 100.0%; Score 502; DB 5; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLAALGLCVALSCSAAFLVGSAPVQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
DB 1 MKLAALGLCVALSCSAAFLVGSAPVQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
QY 61 LSSGIPVNHLEGSQKVAELGQAVGAVKALKALLGALTVEG 104
DB 61 LSSGIPVNHLEGSQKVAELGQAVGAVKALKALLGALTVEG 104

RESULT 6
ABUS8095
ID ABUS8095 standard; protein; 104 AA.
XX
AC ABUS8095;
XX
DT 14-APR-2003 (first entry)
XX
XX Human PRO polypeptide #127.
XX
XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
XX horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
XX antibody-dependent enzyme mediated prodrug therapy.
XX
XX Homo sapiens.
XX
XX US2003027163-A1.
XX
XX 06-FEB-2003.
XX
XX 15-NOV-2001; 2001US-00997666.
XX
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0066770P.
XX 25-FEB-1998; 98US-0075945P.
XX 20-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 03-JUN-1998; 98US-0087759P.
XX 04-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088026P.
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04-JUN-1998; 98US-0088326P.
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05-JUN-1998; 98US-0088940P.
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05-JUN-1998; 98US-0089514P.
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05-JUN-1998; 98US-0089598P.
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05-JUN-1998; 98US-0089600P.
05-JUN-1998; 98US-0089653P.
05-JUN-1998; 98US-0089801P.
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05-JUN-1998; 98US-0089947P.
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05-JUN-1998; 98US-0090445P.
05-JUN-1998; 98US-0090472P.
05-JUN-1998; 98US-0090535P.
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05-JUN-1998; 98US-0090676P.
05-JUN-1998; 98US-0090678P.
05-JUN-1998; 98US-0090690P.
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05-JUN-1998; 98US-0090695P.
05-JUN-1998; 98US-0090696P.
05-JUN-1998; 98US-0090862P.
05-JUN-1998; 98US-0090863P.
05-JUN-1998; 98US-0091360P.
05-JUN-1998; 98US-0091544P.
05-JUN-1998; 98US-0091478P.
05-JUN-1998; 98US-0091519P.
05-JUN-1998; 98US-0091626P.
05-JUN-1998; 98US-0091628P.
05-JUN-1998; 98US-0091633P.
05-JUN-1998; 98US-0091646P.
05-JUN-1998; 98US-0091673P.
05-JUN-1998; 98US-0091978P.
05-JUN-1998; 98US-0091982P.
05-JUN-1998; 98US-0092182P.
05-JUN-1998; 98US-0092472P.
05-JUN-1998; 98US-0093339P.
05-JUN-1998; 98US-0094651P.
05-JUN-1998; 98US-0094651P.

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PR 04-JUN-1998; 98US-0088021P.  
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PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088036P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 12-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089633P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 06-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
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PR 17-MAY-2000; 2000WO-US013705.  
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PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US033678.

28-FEB-2001; 2001WO-US006520.  
01-JUN-2001; 2001WO-US017800.  
20-JUN-2001; 2001WO-US019692.  
29-JUN-2001; 2001WO-US021066.  
09-JUL-2001; 2001WO-US021735.  
28-AUG-2001; 2001US-00941992.  
(GETH ) GENENTECH INC.  
Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
Ferrara N, Fong S, Gerber H, Gertsen ME, Goddard A, Godowski PJ;  
Grimaldi JC, Gurney AL, Kijavini LJ, Napier MA, Pan J, Paoni NF;  
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
Zhang Z;  
WPI; 2003-247083/24.  
N-PSDB; ABX80385.  
Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
are therapeutically useful for enhancing immune response and in cancer  
treatments.  
Claim 12; Fig 290; 648pp; English.  
The invention describes an isolated human PRO polypeptide. The PRO  
polypeptides are useful in detecting PRO polypeptides in a sample, in  
linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
in modulating at least one biological activity of a cell expressing a PRO  
polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
useful for treating cardiac insufficiency disorders. PRO1154 and PRO186  
stimulate adrenal cortical capillary endothelial growth, and PRO536,  
PRO943, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
useful for treating conditions or disorders where angiogenesis would be  
beneficial, e.g. wound healing and antagonist of this polypeptide are  
useful for treating cancerous tumours. PRO812 inhibits vascular  
endothelial growth factor (VEGF) stimulated proliferation of endothelial  
cells and is thus useful for inhibiting endothelial cell growth in  
mammals which would be beneficial in inhibiting tumour growth. PRO826,  
PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
stimulated T-lymphocytes and are therapeutically useful for enhancing  
immune response. PRO826, PRO1068 or PRO132 enhance survival of  
retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
rod photoreceptor cells) and therefore are useful for treating retinal  
disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
and PRO11066 induce proliferation of mammalian kidney mesangial cells,  
and therefore are useful for treating kidney disorders associated with  
decreased mesangial cell function such as Berger disease or other  
nephropathies associated with dermatitis, herpetiformis or Crohn's  
disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
proliferation and/or redifferentiation of chondrocytes in culture and are  
thus useful for treating sports injuries, and arthritis. This is the  
amino acid sequence of a novel human PRO protein

PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
(GETH ) GENENTECH INC.  
PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX Ferrera N, Fong S, Gerber H, Gertsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavini LJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX WPI; 2003-247083/24.  
DR N-PSDB; ABX80385.  
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments.  
XX Claim 12; Fig 290; 648pp; English.  
PS The invention describes an isolated human PRO polypeptide. The PRO  
XX polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO186  
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
CC PRO943, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancerous tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO826, PRO1068 or PRO132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpetiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and are  
CC thus useful for treating sports injuries, and arthritis. This is the  
CC amino acid sequence of a novel human PRO protein  
XX Sequence 104 AA;  
SQ Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLAALLGLCVALLSCSSAAFLVGSAPVAPVAALESAAAGAGTLANPLGTLNPKLL 60  
Db 1 MKLAALLGLCVALLSCSSAAFLVGSAPVAPVAALESAAAGAGTLANPLGTLNPKLL 60  
QY 61 LSSGLIPVNHLEGSQKCVAEIGPQAVGAVKALKALLGALTVEG 104  
Db 61 LSSGLIPVNHLEGSQKCVAEIGPQAVGAVKALKALLGALTVEG 104  
RESULT 8  
ABU82685  
ID ABU82685 standard; protein; 104 AA.

Thu Jun 3 10:25:05 2004

us-09-700-770-9.rag

XX AC AB082685; 19-JUN-1998; 98US-0089948P.  
XX XX 22-JUN-1998; 98US-0089952P.  
XX DT 22-JUN-1998; 98US-0090246P.  
XX XX 22-JUN-1998; 98US-0090252P.  
XX DE 22-JUN-1998; 98US-0090254P.  
XX XX 23-JUN-1998; 98US-0090349P.  
XX XX 23-JUN-1998; 98US-0090355P.  
XX XX 24-JUN-1998; 98US-0090429P.  
XX XX 24-JUN-1998; 98US-0090431P.  
XX XX 24-JUN-1998; 98US-0090435P.  
XX XX 24-JUN-1998; 98US-0090444P.  
XX XX 24-JUN-1998; 98US-0090445P.  
XX XX 24-JUN-1998; 98US-0090472P.  
XX XX 24-JUN-1998; 98US-0090535P.  
XX XX 24-JUN-1998; 98US-0090540P.  
XX XX 24-JUN-1998; 98US-0090542P.  
XX OS 24-JUN-1998; 98US-0090557P.  
XX XX 25-JUN-1998; 98US-0090676P.  
XX PN 25-JUN-1998; 98US-0090678P.  
XX XX 25-JUN-1998; 98US-0090690P.  
XX PD 25-JUN-1998; 98US-0090694P.  
XX XX 25-JUN-1998; 98US-0090695P.  
XX XX 25-JUN-1998; 98US-0090696P.  
XX XX 26-JUN-1998; 98US-0090862P.  
XX XX 01-JUL-1998; 98US-0091360P.  
XX XX 01-JUL-1998; 98US-0091544P.  
XX XX 02-JUL-1998; 98US-0091478P.  
XX XX 02-JUL-1998; 98US-0091519P.  
XX XX 02-JUL-1998; 98US-0091626P.  
XX XX 02-JUL-1998; 98US-0091628P.  
XX XX 02-JUL-1998; 98US-0091633P.  
XX XX 02-JUL-1998; 98US-0091646P.  
XX XX 02-JUL-1998; 98US-0091673P.  
XX XX 07-JUL-1998; 98US-0091978P.  
XX XX 07-JUL-1998; 98US-0091982P.  
XX XX 09-JUL-1998; 98US-0092182P.  
XX XX 10-JUL-1998; 98US-0092472P.  
XX XX 20-JUL-1998; 98US-0093339P.  
XX XX 30-JUL-1998; 98US-0094651P.  
XX XX 04-AUG-1998; 98US-0095282P.  
XX XX 04-AUG-1998; 98US-0095285P.  
XX XX 04-AUG-1998; 98US-0095301P.  
XX XX 04-AUG-1998; 98US-0095302P.  
XX XX 04-AUG-1998; 98US-0095318P.  
XX XX 04-AUG-1998; 98US-0095321P.  
XX XX 04-AUG-1998; 98US-0095325P.  
XX XX 10-AUG-1998; 98US-0095916P.  
XX XX 10-AUG-1998; 98US-0095929P.  
XX XX 10-AUG-1998; 98US-0096012P.  
XX XX 11-AUG-1998; 98US-0096143P.  
XX XX 11-AUG-1998; 98US-0096146P.  
XX XX 12-AUG-1998; 98US-0096329P.  
XX XX 17-AUG-1998; 98US-0096757P.  
XX XX 17-AUG-1998; 98US-0096766P.  
XX XX 17-AUG-1998; 98US-0096768P.  
XX XX 17-AUG-1998; 98US-0096773P.  
XX XX 17-AUG-1998; 98US-0096791P.  
XX XX 17-AUG-1998; 98US-0096867P.  
XX XX 17-AUG-1998; 98US-0096891P.  
XX XX 17-AUG-1998; 98US-0096895P.  
XX XX 17-AUG-1998; 98US-0096897P.  
XX XX 18-AUG-1998; 98US-0096949P.  
XX XX 18-AUG-1998; 98US-0096950P.  
XX XX 18-AUG-1998; 98US-0096959P.  
XX XX 18-AUG-1998; 98US-0096960P.  
XX XX 18-AUG-1998; 98US-0097022P.  
XX XX 19-AUG-1998; 98US-0097141P.  
XX XX 20-AUG-1998; 98US-0097218P.  
XX XX 24-AUG-1998; 98US-0097661P.  
XX XX 26-AUG-1998; 98US-0097952P.  
XX XX 26-AUG-1998; 98US-0097954P.  
  
PR 19-JUN-1998; 98US-0089948P.  
PR 19-JUN-1998; 98US-0089952P.  
PR 22-JUN-1998; 98US-0090246P.  
PR 22-JUN-1998; 98US-0090252P.  
PR 22-JUN-1998; 98US-0090254P.  
PR 23-JUN-1998; 98US-0090349P.  
PR 23-JUN-1998; 98US-0090355P.  
PR 24-JUN-1998; 98US-0090429P.  
PR 24-JUN-1998; 98US-0090431P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
PR 24-JUN-1998; 98US-0090445P.  
PR 24-JUN-1998; 98US-0090472P.  
PR 24-JUN-1998; 98US-0090535P.  
PR 24-JUN-1998; 98US-0090540P.  
PR 24-JUN-1998; 98US-0090542P.  
PR 24-JUN-1998; 98US-0090557P.  
PR 25-JUN-1998; 98US-0090676P.  
PR 25-JUN-1998; 98US-0090678P.  
PR 25-JUN-1998; 98US-0090690P.  
PR 25-JUN-1998; 98US-0090694P.  
PR 25-JUN-1998; 98US-0090695P.  
PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-0090862P.  
PR 01-JUL-1998; 98US-0091360P.  
PR 01-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091519P.  
PR 02-JUL-1998; 98US-0091626P.  
PR 02-JUL-1998; 98US-0091628P.  
PR 02-JUL-1998; 98US-0091633P.  
PR 02-JUL-1998; 98US-0091646P.  
PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
PR 07-JUL-1998; 98US-0091982P.  
PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 04-AUG-1998; 98US-0095285P.  
PR 04-AUG-1998; 98US-0095301P.  
PR 04-AUG-1998; 98US-0095302P.  
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PR 04-AUG-1998; 98US-0095321P.  
PR 04-AUG-1998; 98US-0095325P.  
PR 10-AUG-1998; 98US-0095916P.  
PR 10-AUG-1998; 98US-0095929P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 11-AUG-1998; 98US-0096143P.  
PR 11-AUG-1998; 98US-0096146P.  
PR 12-AUG-1998; 98US-0096329P.  
PR 17-AUG-1998; 98US-0096757P.  
PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096768P.  
PR 17-AUG-1998; 98US-0096773P.  
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PR 17-AUG-1998; 98US-0096895P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
  
Human secreted/transmembrane protein PR01245.  
Human; PRO; secreted protein; transmembrane protein;  
cardiac insufficiency disorders; angiogenesis; wound healing;  
cancerous tumour; immune response; retinal disorder; sight loss;  
retinitis pigmentosum; age-related macular degeneration; AMD;  
kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;  
Crohn's disease; sports injury; arthritis.  
Homo sapiens.  
US2003032023-A1.  
13-FEB-2003.  
14-NOV-2001; 2001US-00990711.  
16-JUN-1997; 97US-0043787P.  
17-OCT-1997; 97US-0062250P.  
05-NOV-1997; 97WO-US020069.  
12-NOV-1997; 97US-0065186P.  
13-NOV-1997; 97US-0065311P.  
24-NOV-1997; 97US-0066770P.  
25-FEB-1998; 98US-0075945P.  
20-MAR-1998; 98US-0078910P.  
28-APR-1998; 98US-0083322P.  
07-MAY-1998; 98US-0084600P.  
28-MAY-1998; 98US-0087106P.  
02-JUN-1998; 98US-0087607P.  
02-JUN-1998; 98US-0087609P.  
03-JUN-1998; 98US-0087759P.  
04-JUN-1998; 98US-0088021P.  
04-JUN-1998; 98US-0088025P.  
04-JUN-1998; 98US-0088026P.  
04-JUN-1998; 98US-0088028P.  
04-JUN-1998; 98US-0088029P.  
04-JUN-1998; 98US-0088030P.  
04-JUN-1998; 98US-0088033P.  
04-JUN-1998; 98US-0088326P.  
05-JUN-1998; 98US-0088167P.  
05-JUN-1998; 98US-0088202P.  
05-JUN-1998; 98US-0088212P.  
05-JUN-1998; 98US-0088217P.  
09-JUN-1998; 98US-0088555P.  
10-JUN-1998; 98US-0088734P.  
10-JUN-1998; 98US-0088738P.  
10-JUN-1998; 98US-0088742P.  
10-JUN-1998; 98US-0088810P.  
10-JUN-1998; 98US-0088824P.  
10-JUN-1998; 98US-0088826P.  
11-JUN-1998; 98US-0088858P.  
11-JUN-1998; 98US-0088861P.  
11-JUN-1998; 98US-0088876P.  
12-JUN-1998; 98US-0089105P.  
16-JUN-1998; 98US-0089440P.  
16-JUN-1998; 98US-0089512P.  
16-JUN-1998; 98US-0089514P.  
17-JUN-1998; 98US-0089532P.  
17-JUN-1998; 98US-0089538P.  
17-JUN-1998; 98US-0089558P.  
17-JUN-1998; 98US-0089599P.  
17-JUN-1998; 98US-0089600P.  
17-JUN-1998; 98US-0089653P.  
18-JUN-1998; 98US-0089801P.  
18-JUN-1998; 98US-0089907P.  
18-JUN-1998; 98US-0089908P.  
19-JUN-1998; 98US-0089947P.

DT 11-AUG-2003 (first entry)  
XX Human uteroglobin related protein 2.  
DE UGRP1; human; mouse; promoter; uteroglobin related protein 1;  
XX respiratory disorder; asthma.  
KW Homo sapiens.  
OS WO2003000111-A2.  
XX 03-JAN-2003.  
PD 18-JUN-2002; 2002WO-US019456.  
PF 20-JUN-2001; 2001US-0299828P.  
XX (USEH ) US DEPT HEALTH & HUMAN SERVICES.  
XX Kimura S, Niimi T;  
XX WPI; 2003-184004/18.  
XX New human UGRP1 nucleic acid, useful for diagnosing or predicting a  
XX predisposition to develop a respiratory disorder or determining the  
XX prognosis of a subject having or suspected of having a respiratory  
XX disorder e.g., asthma.  
XX Disclosure; Page 79-80; 83pp; English.  
XX The present invention provides the human and murine uteroglobin related  
XX protein 1 (UGRP1) promoters. The sequences can be used in the diagnosis  
XX of and prediction of predisposition to respiratory disorders such as  
XX asthma. The present sequence is a protein sequence shown in the  
XX exemplification of the invention  
SQ Sequence 104 AA;  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLAALLGLCVALLSCSSAAAFVGSAPVAPVAALESAAEAGAGTIANPLGTINPLKLL 60  
DB 1 MKLAALLGLCVALLSCSSAAAFVGSAPVAPVAALESAAEAGAGTIANPLGTINPLKLL 60  
QY 61 LSSLGIPVNHLEGSQKCVAEIGPQAVGAVKALKALLGALTIVFG 104  
DB 61 LSSLGIPVNHLEGSQKCVAEIGPQAVGAVKALKALLGALTIVFG 104  
RESULT 1)  
ABU50604 standard; protein; 104 AA.  
XX AC ABU50604;  
XX DT 01-MAY-2003 (first entry)  
XX Human secreted/transmembrane protein, #163.  
XX Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;  
XX diagnostic; therapeutic; gene therapy.  
XX Homo sapiens.  
XX US2002160384-A1.  
XX 31-OCT-2002.  
XX PD 14-NOV-2001; 2001US-00992598.  
XX PF 16-JUN-1997; 97US-0049787P.  
XX PR

PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98US-0100858P.  
PR 07-OCT-1998; 98US-0100858P.  
PR 01-DEC-1998; 98US-0100858P.  
PR 22-DEC-1998; 98US-0100858P.  
PR 05-JAN-1999; 98US-0100858P.  
PR 08-MAR-1999; 98US-0100858P.  
PR 12-MAR-1999; 98US-0100858P.  
PR 02-JUN-1999; 98US-0100858P.  
PR 23-JUN-1999; 98US-0100858P.  
PR 07-JUL-1999; 98US-0100858P.  
PR 20-JUL-1999; 98US-0100858P.  
PR 26-JUL-1999; 98US-0100858P.  
PR 28-JUL-1999; 98US-0100858P.  
PR 17-AUG-1999; 98US-0100858P.  
PR 15-SEP-1999; 98US-0100858P.  
PR 15-SEP-1999; 98US-0100858P.  
PR 08-OCT-1999; 98US-0100858P.  
PR 30-NOV-1999; 98US-0100858P.  
PR 01-DEC-1999; 98US-0100858P.  
PR 01-DEC-1999; 98US-0100858P.  
PR 16-DEC-1999; 98US-0100858P.  
PR 20-DEC-1999; 98US-0100858P.  
PR 05-JAN-2000; 98US-0100858P.  
PR 06-JAN-2000; 98US-0100858P.  
PR 11-FEB-2000; 98US-0100858P.  
PR 18-FEB-2000; 98US-0100858P.  
PR 22-FEB-2000; 98US-0100858P.  
PR 24-FEB-2000; 98US-0100858P.  
PR 24-FEB-2000; 98US-0100858P.  
PR 02-MAR-2000; 98US-0100858P.  
PR 10-MAR-2000; 98US-0100858P.  
PR 15-MAR-2000; 98US-0100858P.  
PR 20-MAR-2000; 98US-0100858P.  
PR 30-MAR-2000; 98US-0100858P.  
PR 15-MAY-2000; 98US-0100858P.  
PR 17-MAY-2000; 98US-0100858P.  
PR 22-MAY-2000; 98US-0100858P.  
PR 30-MAY-2000; 98US-0100858P.  
PR 02-JUN-2000; 98US-0100858P.  
PR 23-JUN-2000; 98US-0100858P.  
PR 28-JUL-2000; 98US-0100858P.  
PR 11-AUG-2000; 98US-0100858P.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLAALLGLCVALLSCSSAAAFVGSAPVAPVAALESAAEAGAGTIANPLGTINPLKLL 60  
DB 1 MKLAALLGLCVALLSCSSAAAFVGSAPVAPVAALESAAEAGAGTIANPLGTINPLKLL 60  
QY 61 LSSLGIPVNHLEGSQKCVAEIGPQAVGAVKALKALLGALTIVFG 104  
DB 61 LSSLGIPVNHLEGSQKCVAEIGPQAVGAVKALKALLGALTIVFG 104  
RESULT 9  
AAO19895 standard; protein; 104 AA.  
XX AC AAO19895;  
XX

PR	17-OCT-1997;	97US-0062250P.	PR	20-MAR-2000;	2000WO-US007377.	PR	20-MAR-2000;	2000WO-US007377.
PR	05-NOV-1997;	97WO-US020069.	PR	30-MAR-2000;	2000WO-US008439.	PR	30-MAR-2000;	2000WO-US008439.
PR	12-NOV-1997;	97US-0065186P.	PR	15-MAY-2000;	2000WO-US013358.	PR	15-MAY-2000;	2000WO-US013358.
PR	13-NOV-1997;	97US-0065311P.	PR	17-MAY-2000;	2000WO-US013705.	PR	17-MAY-2000;	2000WO-US013705.
PR	24-NOV-1997;	97US-0066770P.	PR	22-MAY-2000;	2000WO-US014042.	PR	22-MAY-2000;	2000WO-US014042.
PR	28-FEB-1998;	98US-0075945P.	PR	30-MAY-2000;	2000WO-US014941.	PR	30-MAY-2000;	2000WO-US014941.
PR	20-MAR-1998;	98US-0078910P.	PR	02-JUN-2000;	2000WO-US015264.	PR	02-JUN-2000;	2000WO-US015264.
PR	28-APR-1998;	98US-0083322P.	PR	28-JUL-2000;	2000WO-US020710.	PR	28-JUL-2000;	2000WO-US020710.
PR	07-MAY-1998;	98US-0084600P.	PR	11-AUG-2000;	2000WO-US022031.	PR	11-AUG-2000;	2000WO-US022031.
PR	28-MAY-1998;	98US-0087106P.	PR	23-AUG-2000;	2000WO-US023522.	PR	23-AUG-2000;	2000WO-US023522.
PR	02-JUN-1998;	98US-0087609P.	PR	24-AUG-2000;	2000WO-US023328.	PR	24-AUG-2000;	2000WO-US023328.
PR	02-JUN-1998;	98US-0087759P.	PR	08-NOV-2000;	2000WO-US030952.	PR	08-NOV-2000;	2000WO-US030952.
PR	03-JUN-1998;	98US-0087827P.	PR	01-DEC-2000;	2000WO-US032678.	PR	01-DEC-2000;	2000WO-US032678.
PR	04-JUN-1998;	98US-0088021P.	PR	28-FEB-2001;	2001WO-US006520.	PR	28-FEB-2001;	2001WO-US006520.
PR	04-JUN-1998;	98US-0088025P.	PR	01-JUN-2001;	2001WO-US017800.	PR	01-JUN-2001;	2001WO-US017800.
PR	04-JUN-1998;	98US-0088026P.	PR	20-JUN-2001;	2001WO-US019692.	PR	20-JUN-2001;	2001WO-US019692.
PR	04-JUN-1998;	98US-0088028P.	PR	29-JUN-2001;	2001WO-US021066.	PR	29-JUN-2001;	2001WO-US021066.
PR	04-JUN-1998;	98US-0088029P.	PR	09-JUL-2001;	2001WO-US021735.	PR	09-JUL-2001;	2001WO-US021735.
PR	04-JUN-1998;	98US-0088030P.	PR	28-AUG-2001;	2001US-00941992.	PR	28-AUG-2001;	2001US-00941992.
PR	04-JUN-1998;	98US-0088033P.	XX			XX		
PR	04-JUN-1998;	98US-0088326P.	XX			XX		
PR	05-JUN-1998;	98US-0088167P.	XX			XX		
PR	05-JUN-1998;	98US-0088202P.	PI	Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;		PI	Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;	
PR	05-JUN-1998;	98US-0088212P.	PI	Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;		PI	Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;	
PR	05-JUN-1998;	98US-0088221P.	PI	Grimaldi JC, Gurney AL, Kljavin IU, Napier MA, Pan J, Paoni NF;		PI	Grimaldi JC, Gurney AL, Kljavin IU, Napier MA, Pan J, Paoni NF;	
PR	05-JUN-1998;	98US-00882217P.	PI	Roy MA, Stewart TA, Tumas D, Watanabe CX, Williams PM, Wood WI;		PI	Roy MA, Stewart TA, Tumas D, Watanabe CX, Williams PM, Wood WI;	
PR	09-JUN-1998;	98US-0088655P.	PI	Zhang Z;		PI	Zhang Z;	
PR	10-JUN-1998;	98US-0088734P.	XX			XX		
PR	10-JUN-1998;	98US-0088738P.	DR	WPI, 2003-288106/28.		DR	WPI, 2003-288106/28.	
PR	10-JUN-1998;	98US-0088742P.	DR	N-FSDP; ABX90363.		DR	N-FSDP; ABX90363.	
PR	10-JUN-1998;	98US-0088810P.	XX			XX		
PR	10-JUN-1998;	98US-0088824P.	PT	New transmembrane polypeptides and nucleic acids encoding the		PT	New transmembrane polypeptides and nucleic acids encoding the	
PR	10-JUN-1998;	98US-0088826P.	PT	polypeptides, useful in gene therapy, in chromosome identification, as		PT	polypeptides, useful in gene therapy, in chromosome identification, as	
PR	11-JUN-1998;	98US-0088858P.	XX	chromosome markers, or in generating probes.		XX	chromosome markers, or in generating probes.	
PR	11-JUN-1998;	98US-0088861P.	XX			XX		
PR	11-JUN-1998;	98US-0088876P.	PS	Claim 12; Fig 290; 650pp; English.		PS	Claim 12; Fig 290; 650pp; English.	
PR	12-JUN-1998;	98US-0089105P.	XX			XX		
PR	16-JUN-1998;	98US-0089440P.	CC	The invention discloses isolated PRO secreted/transmembrane polypeptides		CC	The invention discloses isolated PRO secreted/transmembrane polypeptides	
PR	16-JUN-1998;	98US-0089512P.	CC	comprising a sequence without signal peptide and the nucleic acid		CC	comprising a sequence without signal peptide and the nucleic acid	
PR	16-JUN-1998;	98US-0089514P.	CC	encoding them. The polypeptides can be used to raise antibodies that		CC	encoding them. The polypeptides can be used to raise antibodies that	
PR	17-JUN-1998;	98US-0089532P.	CC	specifically bind to the PRO polypeptide, for linking a bioactive		CC	specifically bind to the PRO polypeptide, for linking a bioactive	
PR	17-JUN-1998;	98US-0089538P.	CC	molecule to a cell expressing a PRO protein and for modulating at least		CC	molecule to a cell expressing a PRO protein and for modulating at least	
PR	17-JUN-1998;	98US-0089598P.	CC	one biological activity of a cell. The PRO polypeptides or		CC	one biological activity of a cell. The PRO polypeptides or	
PR	17-JUN-1998;	98US-0089599P.	CC	polynucleotides are also useful in gene therapy, in chromosome		CC	polynucleotides are also useful in gene therapy, in chromosome	
PR	17-JUN-1998;	98US-0089600P.	CC	identification, as chromosome markers, or in generating probes. The PRO		CC	identification, as chromosome markers, or in generating probes. The PRO	
PR	18-JUN-1998;	98US-0089653P.	CC	polypeptides are useful as molecular markers for protein electrophoresis,		CC	polypeptides are useful as molecular markers for protein electrophoresis,	
PR	18-JUN-1998;	98US-0089901P.	CC	and the isolated nucleic acids may be used for recombinantly expressing		CC	and the isolated nucleic acids may be used for recombinantly expressing	
PR	18-JUN-1998;	98US-0089907P.	CC	tissue typing. Anti-PRO antibodies are useful in diagnostic assays for		CC	tissue typing. Anti-PRO antibodies are useful in diagnostic assays for	
PR	16-SEP-1998;	98WO-US019330.	CC	PRO, and in affinity purification of PRO from recombinant cell culture or		CC	PRO, and in affinity purification of PRO from recombinant cell culture or	
PR	17-SEP-1998;	98WO-US019437.	CC	natural sources. The sequences presented in ABU60478-ABU60624 are the PRO		CC	natural sources. The sequences presented in ABU60478-ABU60624 are the PRO	
PR	07-OCT-1998;	98WO-US021141.	CC	polynucleotides of the invention. Note: The sequence data for this patent		CC	polynucleotides of the invention. Note: The sequence data for this patent	
PR	01-DEC-1998;	98WO-US025108.	CC	is also available in electronic format from USPTO at		CC	is also available in electronic format from USPTO at	
PR	05-JAN-1999;	98WO-US000106.	XX	seqdata.uspto.gov/sequence.html		XX	seqdata.uspto.gov/sequence.html	
PR	08-MAR-1999;	98WO-US005028.	SQ	Sequence 104 AA;		SQ	Sequence 104 AA;	
PR	02-JUN-1999;	98WO-US012252.		Query Match 100.0%; Score 502; DB 6; Length 104;			Query Match 100.0%; Score 502; DB 6; Length 104;	
PR	15-SEP-1999;	98WO-US021090.		Best Local Similarity 100.0%; Pred. No. 1.4e-48;			Best Local Similarity 100.0%; Pred. No. 1.4e-48;	
PR	15-SEP-1999;	98WO-US021547.		Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
PR	30-NOV-1999;	99WO-US028313.	QY	1 MKLAALLGLCVALS		QY	1 MKLAALLGLCVALS	
PR	01-DEC-1999;	99WO-US028301.	Db	1 MKLAALLGLCVALS		Db	1 MKLAALLGLCVALS	
PR	01-DEC-1999;	99WO-US028634.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	
PR	16-DEC-1999;	99WO-US030095.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	
PR	20-DEC-1999;	99WO-US030911.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	
PR	05-JAN-2000;	2000WO-US000219.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	
PR	06-JAN-2000;	2000WO-US000376.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	
PR	11-FEB-2000;	2000WO-US0003565.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	
PR	18-FEB-2000;	2000WO-US0004341.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	
PR	22-FEB-2000;	2000WO-US004414.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	
PR	24-FEB-2000;	2000WO-US004914.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	
PR	24-FEB-2000;	2000WO-US005004.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	
PR	02-MAR-2000;	2000WO-US005941.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	
PR	10-MAR-2000;	2000WO-US006319.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	
PR	15-MAR-2000;	2000WO-US006884.		1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104			1 LSSLGIPVNHLEGGSKVVAELGPGQAVGAVKALKALLGALTVEFG 104	

RESULT 11  
ABU1398f  
ID ABU13986 standard; protein; 104 AA.

XX AC ABU13986;  
 XX DT 26-FEB-2003 (first entry)  
 XX DE Human PRO1245 polypeptide.  
 XX KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
 KW genetic disorder; antibacterial; immunosuppressive.  
 XX OS Homo sapiens.  
 XX PN US2002103125-A1.  
 XX DD 01-AUG-2002.  
 XX PF 20-NOV-2001; 2001US-00989731.  
 XX PR 16-JUN-1997; 97US-0049787P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 05-NOV-1997; 97WO-US020069.  
 PR 12-NOV-1997; 97US-0085186P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 25-FEB-1998; 98US-0075945P.  
 PR 20-MAR-1998; 98US-0078910P.  
 PR 28-APR-1998; 98US-0083322P.  
 PR 07-MAY-1998; 98US-0084600P.  
 PR 28-MAY-1998; 98US-0087106P.  
 PR 02-JUN-1998; 98US-0087607P.  
 PR 02-JUN-1998; 98US-0087609P.  
 PR 02-JUN-1998; 98US-0087759P.  
 PR 03-JUN-1998; 98US-0087827P.  
 PR 04-JUN-1998; 98US-0088021P.  
 PR 04-JUN-1998; 98US-0088025P.  
 PR 04-JUN-1998; 98US-0088026P.  
 PR 04-JUN-1998; 98US-0088028P.  
 PR 04-JUN-1998; 98US-0088029P.  
 PR 04-JUN-1998; 98US-0088030P.  
 PR 04-JUN-1998; 98US-0088033P.  
 PR 04-JUN-1998; 98US-0088326P.  
 PR 05-JUN-1998; 98US-0088167P.  
 PR 05-JUN-1998; 98US-0088202P.  
 PR 05-JUN-1998; 98US-0088212P.  
 PR 05-JUN-1998; 98US-0088217P.  
 PR 09-JUN-1998; 98US-0088653P.  
 PR 10-JUN-1998; 98US-0088734P.  
 PR 10-JUN-1998; 98US-0088738P.  
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 PR 10-JUN-1998; 98US-0088824P.  
 PR 10-JUN-1998; 98US-0088828P.  
 PR 11-JUN-1998; 98US-0088858P.  
 PR 11-JUN-1998; 98US-0088861P.  
 PR 11-JUN-1998; 98US-0088876P.  
 PR 12-JUN-1998; 98US-0089105P.  
 PR 16-JUN-1998; 98US-0089440P.  
 PR 16-JUN-1998; 98US-0089512P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 17-JUN-1998; 98US-0089532P.  
 PR 17-JUN-1998; 98US-0089538P.  
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 PR 17-JUN-1998; 98US-0089599P.  
 PR 17-JUN-1998; 98US-0089600P.  
 PR 17-JUN-1998; 98US-0089653P.  
 PR 18-JUN-1998; 98US-0089801P.  
 PR 18-JUN-1998; 98US-0089907P.  
 PR 18-JUN-1998; 98US-0089908P.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 07-OCT-1998; 98WO-US021141.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 06-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019892.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 XX (GETH ) GENENTECH LTD.  
 XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;  
 PI Zhang Z;  
 XX WPI; 2003-102117/09.  
 DR N-P3DB; ABX64209.  
 XX Noval secreted and transmembrane polypeptide for modulating biological  
 PT activity of cell expressing the polypeptide, identifying agonists or  
 PT antagonists of polypeptide, and as molecular weight markers.  
 XX Claim 12; Fig 290; 649pp; English.  
 XX The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for linking  
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
 CC biological activities of cells expressing PRO polypeptides, and for  
 CC identifying agonists or antagonists. The polynucleotide sequences  
 CC encoding PRO polypeptides are useful as hybridisation probes, in  
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,  
 CC in the preparation of PRO polypeptides, for generating transgenic animals  
 CC or knockout animals, to construct hybridisation probes for mapping the  
 CC gene which encodes the PRO polypeptide, and for the genetic analysis of  
 CC individuals with genetic disorders, in gene therapy, for chromosome  
 CC identification, as chromosome markers, and for generating probes for PCR,  
 CC Northern analysis, Southern analysis and Western analysis. ABU13860-  
 CC ABU14006 represent the human PRO polypeptides of the invention. Note: The  
 CC sequence data for this patent was obtained in electronic format directly



Thu Jun 3 10:25:05 2004

us-09-700-770-9.rag

CC from the USPTO web site at seqdata.uspto.gov/psipsdIDEntry.html

XX SQ Sequence 104 AA;

Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAALLGLCVALSCTSSAAAFVLSAKPVAQPVAALESAAAGAGTLANPLGTINPLKLL 60  
DB 1 MKLAALLGLCVALSCTSSAAAFVLSAKPVAQPVAALESAAAGAGTLANPLGTINPLKLL 60  
QY 61 LSSLGIPVNHLEIGSKQKVAELGPOAVGAVKALKALLGALTTFVG 104  
DB 61 LSSLGIPVNHLEIGSKQKVAELGPOAVGAVKALKALLGALTTFVG 104

RESULT 12

ABU72571

ID ABU72571 standard; protein; 104 AA.

XX AC ABU72571;

XX DT 17-JUN-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO1245.

KW Human; secreted and transmembrane protein; cytostatic; anti-HIV;  
KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;  
KW PRO; pharmaceutical; diagnostic; biosensor; bio-reactor; malignancy;  
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;  
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;  
KW drug screening.

XX OS Homo sapiens.

XX PN US2003003531-A1.

XX PD 02-JAN-2003.

XX PF 19-NOV-2001; 2001US-00989734.

XX PR 16-JUN-1997; 97US-0049787P.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 05-NOV-1997; 97WO-US020069.

XX PR 12-NOV-1997; 97US-0065186P.

XX PR 13-NOV-1997; 97US-0065311P.

XX PR 24-NOV-1997; 97US-0066770P.

XX PR 25-FEB-1998; 98US-0075945P.

XX PR 20-MAR-1998; 98US-0078910P.

XX PR 28-APR-1998; 98US-0083322P.

XX PR 07-MAY-1998; 98US-0084600P.

XX PR 28-MAY-1998; 98US-0087106P.

XX PR 02-JUN-1998; 98US-0087607P.

XX PR 02-JUN-1998; 98US-0087609P.

XX PR 02-JUN-1998; 98US-0087759P.

XX PR 03-JUN-1998; 98US-0087827P.

XX PR 04-JUN-1998; 98US-0088021P.

XX PR 04-JUN-1998; 98US-0088025P.

XX PR 04-JUN-1998; 98US-0088026P.

XX PR 04-JUN-1998; 98US-0088028P.

PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089588P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.

(GETH ) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;  
XX PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
XX PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;  
XX PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
XX PI Zhang Z;

XX WFI; 2003-352829/33.  
DR N-FSDB; ACA64431.

XX New genes and secreted and transmembrane polypeptides (e.g. PRO183 or  
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's  
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's  
PT disease.  
XX  
XX  
PS Claim 12; Fig 290; 663pp; English.  
XX  
XX The invention describes a new isolated nucleic acid molecule comprising  
CC the full length coding sequence of the DNA deposited with the American  
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,  
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA  
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are  
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These  
CC are particularly useful for detecting or treating e.g. malignancies or  
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,  
CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's  
CC disease in mammals. The PRO polypeptides are useful in drug screening,  
CC particularly as targets for therapeutic intervention in these diseases,  
CC and in the diagnostic determination of the presence of these diseases.  
CC The PRO polypeptides are also useful as molecular weight markers, or for  
CC chromosome identification. The PRO genes are useful as hybridisation  
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.  
CC The PRO genes may also be used in gene therapy, particularly for  
CC replacing a defective gene. This is the amino acid sequence of a novel  
CC human secreted and transmembrane PRO polypeptide  
XX  
XX Sequence 104 AA;  
SQ

Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLAALLGLCVALLSCSSAAFLVGSAPVAPVVALESAAEAGCTLANPLGTLNPKLL 60  
Db 1 MKLAALLGLCVALLSCSSAAFLVGSAPVAPVVALESAAEAGCTLANPLGTLNPKLL 60

Qy 61 LSSGIPVNHILEGSKVCAELGPOAVGAVKALKALLGALTIVFG 104  
Db 61 LSSGIPVNHILEGSKVCAELGPOAVGAVKALKALLGALTIVFG 104

RESULT 13  
ABU59320  
ID ABU59320 standard; protein; 104 AA.  
XX  
XX AC ABU59320;  
XX  
XX DT 22-APR-2003 (first entry)  
XX  
XX DE Human secreted/transmembrane protein, #163.  
XX  
XX KW Human; PRO; secreted; transmembrane; pharmaceutical; diagnostic;  
KW biosensor; bioreactor; tumour; therapeutic; gene therapy;  
KW tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
XX  
XX OS Homo sapiens.  
XX  
XX PN US2003027162-A1.  
XX  
XX PD 06-FEB-2003.  
XX  
XX PF 15-NOV-2001; 2001US-00997428.  
XX  
XX PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
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PR 02-JUN-1998; 98US-0087607P.  
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PR 02-JUN-1998; 98US-0087759P.  
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PR 09-JUN-1998; 98US-0088555P.  
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PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
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PR 12-JUN-1998; 98US-0089105P.  
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PR 19-JUN-1998; 98US-0089952P.  
PR 22-JUN-1998; 98US-0090246P.  
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PR 24-JUN-1998; 98US-0090429P.  
PR 24-JUN-1998; 98US-0090431P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
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PR 24-JUN-1998; 98US-0090472P.  
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PR 24-JUN-1998; 98US-0090540P.  
PR 24-JUN-1998; 98US-0090572P.  
PR 25-JUN-1998; 98US-0090676P.  
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PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 01-JUL-1998; 98US-0091360P.  
PR 01-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091519P.  
PR 02-JUL-1998; 98US-0091626P.



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PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 05-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089633P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021030.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005044.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.

PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 03-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kijavini LJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
XX WPI; 2003-340824/32.
DR N-PEDB; ACD44399.
XX
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT and are therapeutically useful for enhancing immune responses.
XX
PS Claim 12; Fig 290; 661pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, and for for-
CC biological activities of cells expressing PRO polypeptides, and for for-
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. ABO25891-
CC ABO26037 represent the human PRO polypeptides of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/psipdidentry.html
XX
SQ Sequence 104 AA;
Query Match 100.0%; Score 502; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLAALLGLCVALLSCSSAAAEFLVGSAPVAPVAALESAAEAGAGTLANPLGTLNPLKLL 60
Db 1 MKLAALLGLCVALLSCSSAAAEFLVGSAPVAPVAALESAAEAGAGTLANPLGTLNPLKLL 60
QY 61 LSSIGIPVNHIIEGSKVCVABLGQVANGAVKALKALGALTIVFG 104
Db 61 LSSIGIPVNHIIEGSKVCVABLGQVANGAVKALKALGALTIVFG 104
RESULT 15
AEUS9026
ID ABUS9026 standard; protein; 104 AA.
XX
XX AC ABUS9026;
XX
XX DT 16-APR-2003 (first entry)
XX
XX DE Human secreted/transmembrane protein, #163.
XX
XX KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
KW diagnostic; biosensor; bioreactor; tumour; therapeutic; colon cancer;
KW lung cancer; breast cancer; cancer; gene therapy.
XX
```



QY 61 LSSLGIPVNHLEIGSOKCVAELGPQAVGAVKALKALLGALTVEG 104  
DB 61 LSSLGIPVNHLEIGSOKCVAELGPQAVGAVKALKALLGALTVEG 104

Search completed: June 2, 2004, 20:19:02  
Job time : 25.778 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:07:29 ; Search time 67.3906 Seconds  
(without alignments)  
1966.411 Million cell updates/sec

Title: US-09-700-770-8  
Perfect score: 2238  
Sequence: 1 MSPPPPLQLLLLLPLLNVE.....ARTRGADLWGGETAQAFPG 420

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mbc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2238	100.0	420	4 Q8WWD9	Q8WWD9 homo sapien
2	1887	84.3	450	4 Q9UBH3	Q9UBH3 homo sapien
3	1566	70.0	420	11 Q9QX71	Q9QX71 rattus norv
4	1551.5	69.3	419	11 Q9DCS8	Q9DCS8 mus musculu
5	1550.5	69.3	419	11 Q9JW79	Q9JW79 mus musculu
6	1025	45.8	399	13 Q93458	Q93458 podarcis si
7	1018.5	45.5	398	13 Q8JH28	Q8JH28 brachydanio
8	1018.5	45.5	398	13 Q8AWD9	Q8AWD9 brachydanio
9	1014.5	45.3	398	13 P87370	P87370 oncornychu
10	1005.5	44.9	392	5 Q9V313	Q9V313 drosophila
11	1005.5	44.9	399	13 Q9DD89	Q9DD89 brachydanio
12	985.5	44.0	396	13 Q93428	Q93428 chionodraco
13	977	43.7	397	13 Q9W6D4	Q9W6D4 hynobius le
14	974	43.5	395	13 Q8J124	Q8J124 silurus aso
15	966.5	43.2	385	5 Q7Z1E4	Q7Z1E4 bombyx mori
16	949.5	42.4	386	6 Q9BGU5	Q9BGU5 bos taurus

17	324.5	41.3	445	11	Q8C243	Q8C243 mus musculu
18	305.5	40.5	444	5	Q21966	Q21966 caenorhabdi
19	897	40.1	446	5	Q86Q14	Q86Q14 ancylostoma
20	890	39.8	386	5	Q8WR56	Q8WR56 apriona ger
21	887	39.6	446	5	Q9N9H3	Q9N9H3 necator ame
22	374.5	39.1	397	13	Q805F2	Q805F2 xenopus lae
23	871	38.9	409	13	Q804Z9	Q804Z9 xenopus lae
24	865.5	38.7	419	5	Q95VA2	Q95VA2 clonorchis
25	864.5	38.6	397	13	Q805F3	Q805F3 xenopus lae
26	859.5	38.4	495	10	Q9LQZ3	Q9LQZ3 oryza sativ
27	848	37.9	397	13	Q800A0	Q800A0 rana catesb
28	847	37.8	399	13	Q57477	Q57477 sparus aua
29	847	37.8	578	10	Q7XB41	Q7XB41 chlamydomon
30	839	37.5	427	5	P91802	P91802 schistosoma
31	829.5	37.1	429	5	Q26515	Q26515 schistosoma
32	828.5	37.0	514	10	Q8L6A9	Q8L6A9 theobroma c
33	827.5	37.0	452	5	Q8MY58	Q8MY58 brugia mala
34	817	36.5	416	13	Q9DDE2	Q9DDE2 brachydanio
35	804.5	35.9	401	11	Q91X66	Q91X66 mus musculu
36	803.5	35.9	442	5	Q93106	Q93106 ancylostoma
37	803.5	35.9	514	10	Q9PRW9	Q9PRW9 nepenthes a
38	799.5	35.7	404	5	Q8MZP3	Q8MZP3 drosophila
39	797.5	35.6	404	5	Q9V717	Q9V717 drosophila
40	795	35.5	514	10	Q94IA2	Q94IA2 glycine max
41	792.5	35.4	512	10	Q04593	Q04593 arabidopsis
42	792	35.4	513	10	Q8VYL3	Q8VYL3 arabidopsis
43	785.5	35.1	406	13	P70068	P70068 pagothenia
44	784.5	35.1	504	10	Q93XR0	Q93XR0 ipomoea bat
45	784	35.0	513	10	Q41713	Q41713 vigna ungui

## ALIGNMENTS

### RESULT 1

Q8WWD9	ID	Q8WWD9	PRELIMINARY;	PRT;	420 AA.
AC	Q8WWD9;				
DT	01-MAR-2002	(Tremblrel. 20, Created)			
DT	01-MAR-2002	(Tremblrel. 20, Last sequence update)			
DT	01-CCT-2003	(Tremblrel. 25, Last annotation update)			
DE	Prorapsin A.				
OS	Homc saptens (Human).				
OC	Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Lung;				
RA	Strausberg R.;				
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.				
DR	EMBL: BC017842; AAH17842.1; -				
DR	GO: GO:0004194; P:pepsin A activity; IEA.				
DR	GO: GO:0008233; P:peptidase activity; IEA.				
DR	GO: GO:0006508; P:proteolysis and peptidolysis; IEA.				
DR	InterPro; IPR001969; Asparticase AS.				
DR	InterPro; IPR001461; Peptidase A1.				
DR	InterPro; IPR009007; Pept_A_acid.				
DR	Pfam; PF00026; asp_1				
DR	PRINTS; PR00792; PEPsin.				
DR	PROSITE; PS00141; ASP_PROTEASE; 2.				
KW	Aspartyl protease; Hydrolase; Protease.				
SQ	SEQUENCE 420 AA; 45374 MW; 05A1B95D68D3F495 CRC64;				

Query Match 100.0%; Score 2238; DB 4; Length 420;  
Best Local Similarity 100.0%; Pred. No. 2e-171;  
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPPPPLQLLLLLPLLNVEPGATLIRIPLHRVQPGRTTLNLRGWREPAELFKLGAPS 60  
DB 1 MSPPPPLQLLLLLPLLNVEPGATLIRIPLHRVQPGRTTLNLRGWREPAELFKLGAPS 60

QY	61	PGDKPIFVPLSNRYDQVQFGEIGLGTTPQNFTVAEDTGSNNLWVPBRRCHFFSVPCWLHH	120
Db	61	PGDKPIFVPLSNRYDQVQFGEIGLGTTPQNFTVAEDTGSNNLWVPBRRCHFFSVPCWLHH	120
QY	121	RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPSSLVFAF	180
Db	121	RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPSSLVFAF	180
QY	181	AHFDGILGLGFPILSVEGVPPMDVLVEQGLDKPVSFYLNDRDPEPDGDELVLGSDP	240
Db	181	AHFDGILGLGFPILSVEGVPPMDVLVEQGLDKPVSFYLNDRDPEPDGDELVLGSDP	240
QY	241	AHYIPPLTFVPTVPAYQWQHMERVKVGPGLTCAKCAAILDTGSLTIGTPEEIRALH	300
Db	241	AHYIPPLTFVPTVPAYQWQHMERVKVGPGLTCAKCAAILDTGSLTIGTPEEIRALH	300
QY	301	AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGLGVWFLNTAHDYVIQTTNRNGVRLCLSGFOA	360
Db	301	AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGLGVWFLNTAHDYVIQTTNRNGVRLCLSGFOA	360
QY	361	LDVPPAGPFWILGDVFLGTGYVAVFDRGDMKSSARVGLARTRGADLGHGETAQAPFG	420
Db	361	LDVPPAGPFWILGDVFLGTGYVAVFDRGDMKSSARVGLARTRGADLGHGETAQAPFG	420
RESULT 2			
ID	Q9UHB3	PRELIMINARY; PRT; 450 AA.	
AC	Q9UHB3		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Aspartyl protease 3 (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
EN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20057170; PubMed=10591213;		
RA	Yan R., Bienkowski M.J., Shuck M.B., Miao H., Tory M.C., Pauley A.M.,		
RA	Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,		
RA	Tonasselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.B.;		
RT	"Membrane-anchored aspartyl protease with Alzheimer's disease beta-		
RT	secretase activity.,"		
RL	Nature 402:533-537(1999).		
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.		
DR	EMBL; AF200344; AAF17080.1; -.		
DR	HSSP; P00794; 4CMS.		
DR	MEROPS; A01.972; -.		
DR	GO; GO:0016020; C:membrane; TAS.		
DR	GO; GO:0004194; F:pepsin A activity; NAS.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; TAS.		
DR	InterPro; IPR001969; Asprotease AS.		
DR	InterPro; IPR001461; Peptidase A1.		
DR	InterPro; IPR009007; Pept_A_acid.		
DR	Pfam; PF00026; asp; 1.		
DR	PRINTS; PR00792; PEPIN.		
DR	PROSITE; PS00141; ASP PROTEASE; 2.		
KW	Aspartyl protease; Hydrolase; Protease.		
FT	NON TER 450		
SQ	SEQUENCE 450 AA; 48576 MW; B7731C85E106C0DD CRC64;		
Query Match			
Best Local Similarity 84.3%; Score 1887; DB 4; Length 450;			
Matches 360; Conservative 16; Mismatches 44; Indels 0; Gaps 0;			
QY	1	MSPPPLQLLLLLPLLNVEPSGATLIRIPHRVQPGRTINLIRGWRPAELPKLGAPS	60
Db	1	MSPPPLQLLLLLPLLNVEPSGATLIRIPHRVQPGRTINLIRGWRPAELPKLGAPS	60
QY	61	PGDKPIFVPLSNRYDQVQFGEIGLGTTPQNFTVAEDTGSNNLWVPBRRCHFFSVPCWLHH	120

Db	61	PGDKPASVLSKFLDAQYFEGELGTPPQNFTVAEDTGSNNLWVPBRRCHFFSVPCWFHH	120
QY	121	RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPSSLVFAF	180
Db	121	RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPSSLVFAF	180
QY	181	AHFDGILGLGFPILSVEGVPPMDVLVEQGLDKPVSFYLNDRDPEPDGDELVLGSDP	240
Db	181	SRPDGILGLGFPILSVEGVPPMDVLVEQGLDKPVSFYLNDRDPEPDGDELVLGSDP	240
QY	241	AHYIPPLTFVPTVPAYQWQHMERVKVGPGLTCAKCAAILDTGSLTIGTPEEIRALH	300
Db	241	AHYIPPLTFVPTVPAYQWQHMERVKVGPGLTCAKCAAILDTGSLTIGTPEEIRALH	300
QY	301	AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGLGVWFLNTAHDYVIQTTNRNGVRLCLSGFOA	360
Db	301	AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGLGVWFLNTAHDYVIQTTNRNGVRLCLSGFOA	360
QY	361	LDVPPAGPFWILGDVFLGTGYVAVFDRGDMKSSARVGLARTRGADLGHGETAQAPFG	420
Db	361	LDIASPPVPWILGDVFLGTGYVAVFDRGDMKSSARVGLARTRGADLGRRETAQAYRG	420
RESULT 3			
ID	Q9QX71	PRELIMINARY; PRT; 420 AA.	
AC	Q9QX71		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Napsin.		
GN	NAP.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
EN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20461778; PubMed=10858550;		
RA	Schauer-Vukasinovic V., Wright M.B., Breu V., Giller T.;		
RT	"Cloning, expression and functional characterization of rat napsin.,"		
RL	Biochim. Biophys. Acta 1492:207-210(2000).		
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.		
DR	EMBL; AJ251299; CAB65392.1; -.		
DR	HSSP; P00797; 2REN.		
DR	MEROPS; A01.049; -.		
DR	GO; GO:0004194; F:pepsin A activity; IEA.		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR001969; Asprotease AS.		
DR	InterPro; IPR001461; Peptidase A1.		
DR	InterPro; IPR009007; Pept_A_acid.		
DR	Pfam; PF00026; asp; 1.		
DR	PRINTS; PR00792; PEPIN		
DR	PROSITE; PS00141; ASP PROTEASE; 2.		
KW	Aspartyl protease; Hydrolase; Protease.		
SQ	SEQUENCE 420 AA; 45629 MW; A6851C6A2F7D8D7C CRC64;		
Query Watch			
Best Local Similarity 70.4%; Score 1566; DB 11; Length 420;			
Matches 299; Conservative 39; Mismatches 77; Indels 10; Gaps 5;			
QY	1	MSPPPLQLLLLLPLLNVEPSGATLIRIPHRVQPGRTINLIRGWRPAELPKLGAP	59
Db	1	MLPPELL--LLLCVLLGNLEPA-ATLIRVPLRIRHPGHRIFSPLYGWEQRAELSR--TP	55
QY	60	SPGDPIFVPLSNRYDQVQFGEIGLGTTPQNFTVAEDTGSNNLWVPBRRCHFFSVPCWLH	119
Db	56	TSGGKTAFAVPLSKFMNTQYFGDIGLTPQNFTVVDGSSNLWVPSRCHFFSLACWFH	115
QY	120	HRFPDKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPSSLVFA	179
Db	116	HRFPDKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPSSLVFA	175



```

QY 180 FAHFDGILGIFPILSVGVRPMDVLVQGLLDKPVFSFYLNDRDPEPDGGLVLGSSD 239
Db 176 LARFDGILGIFPILSVGVRPMDVLVQGLLDKPVFSFYLNDRDPEPDGGLVLGSSD 235
QY 240 PAHYIPLPFTVPVTPAYVQIMHMERVKVGFGLTLCAGCAALDGTSLTGTTEIRAL 299
Db 236 PDHYVPLPFTVPVTPAYVQIMHMERVKVGFGLTLCAGCAALDGTSLTGTTEIRAL 295
QY 300 HAAIGIPILAGHYIILCSBIPKLPVAVSFLGGLGWNLTAHDYVQITTRNGVPLCLSGFQ 359
Db 296 NKAVGFPILGTYLLQCSKIPBLPTVFSGLGWNLTAHDYVQITTRNGVPLCLSGFQ 355
QY 360 ALDVPVPPAGFWILGDFVLTGYVAVFDRGDMKSSARVGLARTRGADLWGSETAQAF 418
Db 356 ALDVPVPPAGFWILGDFVLTGYVAVFDRGDMKSSARVGLARTRGADLWGSETAQAF 415
QY 419 ---PG 420
Db 416 RRRPG 420

RESULT 4
Q9DCS8 PRELIMINARY; PRT; 419 AA.
AC Q9DCS8;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Kidney-derived aspartic protease-like protein.
GN KDAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana S.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schram L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., King B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wyszak H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaehizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR EMBL; AK002520; BAB2158.1; -.
DR HSP; P00797; 2REN.
DR MGD; MGI:109365; Kdap.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001969; Aspartic protease AS.
DR InterPro; IPR001461; Peptidase A1.
DR InterPro; IPR009007; Pept_A acid.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Aspartyl protease; Hydrolase; Protease.

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SQ SEQUENCE 419 AA; 45504 MW; 715EC5472280003B CRC64;
Query Match 69.3%; Score 1551.5; DB 11; Length 419;
Best Local Similarity 70.1%; Pred. No. 2.7e-116;
Matches 295; Conservative 37; Mismatches 80; Indels 9; Gaps 3;
QY 7 LQPLLLLLPFL---NVPSGATLIRPLHRVQPGRTTLLNLGRWREPAPLKLGAESPQD 63
Db 1 MSPLLLLLLLLGNNLEPEAKLIRVPLQRIHLGRIILNPLNGWEQLAELSR--TSTGG 58
QY 64 KFIPLVSNYRDVQVGEIGLCTPPQNFVADTSSNLWVPSRRCHFFSPVCLWHRFD 123
Db 59 NPSFVPLSKFMNTQVFTGLTTPQNFVADTSSNLWVPSRRCHFFSLACWFHFRN 118
QY 124 PRASSFOANGTKFAIOYGTGRVDGLISBDKLTIGGKGVIFGREALWEPISVFAFAHF 183
Db 119 PRASSFRNGTKFAIOYGTGRISGLSDNLTIGGIHDAFTVFGREALWEPISLIFALAHF 178
QY 184 DGIPLGFPILSVGVRPMDVLVQGLLDKPVFSFYLNDRDPEPDGGLVLGSSDPAHY 243
Db 179 DGIPLGFPILSVGVRPMDVLVQGLLDKPVFSFYLNDRDPEPDGGLVLGSSDPAHY 238
QY 244 IPLPFTVPVTPAYVQIMHMERVKVGFGLTLCAGCAALDGTSLTGTTEIRALHAAL 303
Db 239 VPELTPFTVPVTPAYVQIMHMERVKVGFGLTLCAGCAALDGTSLTGTTEIRALHAAL 298
QY 304 GGIPLLAGHYIILCSBIPKLPVAVSFLGGLGWNLTAHDYVQITTRNGVPLCLSGFOALDV 363
Db 299 GGYPLNGQVFFQCKTPTLPVSVFHLGGLGWNLTAHDYVQITTRNGVPLCLSGFOALDI 358
QY 364 PPPAGFPWILGDFVLTGYVAVFDRGDMKSSARVGLARTRGADLWGSETAQAF----P 419
Db 359 PNAAGPLWILGDFVLTGYVAVFDRGDMKSSARVGLARTRGADLWGSETAQAF----P 418
QY 420 G 420
Db 419 G 419

RESULT 5
Q9JW79 PRELIMINARY; PRT; 419 AA.
AC Q9JW79;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Aspartic proteinase family member similar to renin.
GN KDAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98168041; PubMed=9507200;
RA Takenaka M., Imai E., Kaneko T., Ito T., Moriyama T., Yamauchi A.,
RA Hori M., Kawamoto S., Okubo K.;
RT "Isolation of genes identified in mouse renal proximal tubule by
RL Kidney Int. 53:562-572(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR EMBL; AB038144; BAA90785.1; -.
DR HSP; P00797; 2REN.
DR MGD; MGI:109365; Kdap.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

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DR GO: 0004194; F:pepsin A activity; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001969; Asparticase AS.
DR InterPro: IPR001461; Peptidase A1.
DR InterPro: IPR009007; Pept_A_acid.
DR Pfam: PF00026; asp; 1.
DR PRINTS: PR00792; PEPSIN.
DR PROSITE: PS00141; ASP_PROTEASE; 2.
KW SIGNAL; Hydrolase.
FT SIGNAL 1 18 POTENTIAL.
SQ SEQUENCE 398 AA; 43171 MW; 2A42FE4239B897F6 CRC64;

Query Match 45.5%; Score 1018.5; DB 13; Length 398;
Best Local Similarity 50.5%; Pred. No. 1.6e-73;
Matches 195; Conservative 65; Mismatches 111; Indels 15; Gaps 4;

QY 26 LRIPLHVPQGRRTINLLRGWREPALP-----KLGAPSPGDKPIFVPLSNRDVQ 77
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
19 IVRIPLKFKFTLRRTLS--DSGRSLEELVSSNSLKNLGFASND-PTPETLKNYLDQA 75
QY 78 YFGEIGLGTTPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSSFOANGTKF 137
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
76 YGEIGLGTVPQFTVFTVDTGSSNLWVPSVHCSLTDIACLLHKKYNGKSSITVKKGTQF 135
QY 138 AIQYGRVDGILSEDKLTIGGKASVIFGEALWEPSPVFAFAHFDGILGLGFPILSVE 197
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
136 AIQYSGSLGYLSQDCTIGDIAVEKQIFGEAIKQPGVAFIAAKFDGILGMAYPRIAVD 195
QY 198 GVRPPMDVLVEQGLLDKPVFSFYLNDRDPEDGGELVLGSDPAHYIPPTFTFVTVTPAY 257
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
196 GVPPFVDMMSQKKVKNVFSFYLNDRPDTQGGELLGGTDPKYTGDFNYVDISRQAY 255
QY 258 WQIHMERVKVPGGLTLCAGCAAILDTGSLTGTPTTEIRALHAAIGGIPLLAGEYIILC 317
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
256 WQIHMDGMSIGSLCKGCEALVDGTSLITGPAAEVKALQKAIPLMGEYIIVDC 315
QY 318 SEIPKLPVAVFLGGVFNLTADHYVIQTRNGVRLCLSGFQALDVPVPPAGPFWILGDVF 377
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
316 KKVPTLPTISFSLGGKVSILTGQYILKESQGGHDCISGFMLGDIPTPPAGPLWILGDVF 375
QY 378 LGTYVAVFDRGDMKSSARVGLARPT 403
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
376 IGQYTVFDR-----ENNRVGFKAQKS 397

RESULT 9
P87370 PRELIMINARY; PRT; 398 AA.
ID AC P87370 PRELIMINARY; PRT; 398 AA.
AC P87370;
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cathepsin D (EC 3.4.23.5).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pre-vitellogenic ovary;
RX MEDLINE=98072428; PubMed=9409770;
RA Brooks S., Tyler C.R., Carnevali O., Coward K., Sumpter J.P.;
RT "Molecular characterisation of ovarian cathepsin D in the rainbow
trout, Oncorhynchus mykiss.";
RL Gene 201:45-54 (1997).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR EMBL; U90321; AAC60301.1; -.
DR HSP; P07339; 1LYB.
DR MEROPS; A01.009; -.
DR GO: 0004192; F:cathepsin D activity; IEA.
DR GO: 0004194; F:pepsin A activity; IEA.
DR GO: 0008233; F:peptidase activity; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001969; Asparticase AS.
DR InterPro: IPR001461; Peptidase A1.
DR InterPro: IPR009007; Pept_A_acid.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Aspartyl protease; Hydrolase; Protease.
SQ SEQUENCE 398 AA; 42973 MW; 23C94FB3F5EC99D9 CRC64;

Query Match 45.3%; Score 1014.5; DB 13; Length 398;
Best Local Similarity 50.6%; Pred. No. 3.4e-73;
Matches 195; Conservative 65; Mismatches 111; Indels 15; Gaps 4;

QY 26 LRIPLHVPQGRRTINLLRGWREPALP-----KLGAPSPGDKPIFVPLSNRDVQ 77
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
19 IVRIPLKFKFTLRRTLS--DSGRSLEELVSSNSLKNLGFASND-PTPETLKNYLDQA 75
QY 78 YFGEIGLGTTPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSSFOANGTKF 137
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
76 YGEIGLGTVPQFTVFTVDTGSSNLWVPSVHCSLTDIACLLHKKYNGKSSITVKKGTQF 135
QY 138 AIQYGRVDGILSEDKLTIGGKASVIFGEALWEPSPVFAFAHFDGILGLGFPILSVE 197
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
136 AIQYSGSLGYLSQDCTIGDIAVEKQIFGEAIKQPGVAFIAAKFDGILGMAYPRIAVD 195
QY 198 GVRPPMDVLVEQGLLDKPVFSFYLNDRDPEDGGELVLGSDPAHYIPPTFTFVTVTPAY 257
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
196 GVPPFVDMMSQKKVKNVFSFYLNDRPDTQGGELLGGTDPKYTGDFNYVDISRQAY 255
QY 258 WQIHMERVKVPGGLTLCAGCAAILDTGSLTGTPTTEIRALHAAIGGIPLLAGEYIILC 317
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
256 WQIHMDGMSIGSLCKGCEALVDGTSLITGPAAEVKALQKAIPLMGEYIIVDC 315
QY 318 SEIPKLPVAVFLGGVFNLTADHYVIQTRNGVRLCLSGFQALDVPVPPAGPFWILGDVF 377
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
316 KKVPTLPTISFSLGGKVSILTGQYILKESQGGHDCISGFMLGDIPTPPAGPLWILGDVF 375
QY 378 LGTYVAVFDRGDMKSSARVGLARPT 403
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
376 IGQYTVFDR-----ENNRVGFKAQKS 397

RESULT 8
Q8AND9 PRELIMINARY; PRT; 398 AA.
AC Q8AND9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to cathepsin D.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC042316; AA042316.1; -.
DR GO: 0004194; F:pepsin A activity; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001969; Asparticase AS.
DR InterPro: IPR001461; Peptidase A1.
DR InterPro: IPR009007; Pept_A_acid.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
SQ SEQUENCE 398 AA; 43199 MW; 2EB897840DEAD6D CRC64;

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QY 379 GTYVAVFDRGDMKSSARVGLAR 402
DB 373 GKYYTEFDMG----NDRVGFADAK 392

RESULT 11
Q9DD89 PRELIMINARY; PRT; 399 AA.
AC Q9DD89
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cathepsin D enzyme (EC 3.4.23.5).
GN CSD OR CATHEPSIN D.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2057889; PubMed=11137292;
RA Riggio M., Scudiero R., Filosa S., Parisi E.;
RT "Sex and tissue-specific expression of aspartic proteinase in Danio
RT rerio (zebrafish).";
RL Gene 260:67-75(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR EMBL; AJ278268; CAC20111.1; -.
DR HSSP; P07339; 11YB.
DR MEROPS; A01.009; -.
DR ZFIN; ZDB-GENE-010131-8; ctsd.
DR GO; GO:0004192; F:cathepsin D activity; IEA.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001969; Asparticase AS.
DR InterPro; IPR001461; Peptidase A1.
DR InterPro; IPR009007; Pept_A_acid.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
DR Aspartyl protease; Hydrolase; Protease.
KW SIGNAL 1 18 POTENTIAL.
FT CHAIN 62 396 CATHEPSIN D.
SQ SEQUENCE 399 AA; 43505 MW; 5A988CA9751B5EEC CRC64;

Query Match 44.9%; Score 1005.5; DB 13; Length 399;
Best Local Similarity 50.8%; Pred. No. 1.8e-72;
Matches 196; Conservative 62; Mismatches 111; Indels 17; Gaps 5;

QY 28 RIPLHVPQGRRTINLLRGWREPAELP-----KLGAQPGDKPIFVPLSNYRDVQYF 79
DB 20 RIPLKXPTLRITLS--DSGSLSELYSSNSLXNLFPPASND-PTETLKNYLDQY 76

QY 80 GEIGLTPPQNTVAFDTGSSNLNVPVRRCHFFSVPCMLHRRFDPKASSFOANGTKPAI 139
DB 77 GEIGLTPVQNTVAFDTGSSNLNVPVRRCHFFSVPCMLHRRFDPKASSFOANGTKPAI 136

QY 140 QYGRVDGILSEDKLTGGIKGASVIFGEALWPSLFAHFGILGLGFPILSVEGV 199
DB 137 QYGSLSGYSLSQDTCTTGDAVEKQIFGEAKIQGVAFIAKFGILGLGMAYPRISVDGV 196

QY 200 RPPMDVLVEQLLDKPFVFLNRPDPDGGELVGGSDPAHYIPPIPTFVPVTPAYWQ 259
DB 197 PVPFDMWSQKKVEKNVFSFLNRPDPDPGELLGGTDPKYYTGDYNDYDISQAYWQ 256

QY 260 IHMERVKVGPGLTLCAGCAAILDTG--TSLITGPTTEIRALHAAIGIPLAGYIILC 317
DB 257 IHMDQMSIGSLGSLCKGGEAIVDTGTSTSLITGPAAEVKALQKAIGAIPLMQGEYMDVC 316

QY 318 SEIPKLPVSLFLLGGVWNLTAHDYVIQTRNGVRLCLSGFALQVPPAGFPWILGVDF 377
DB 317 KKVPTLPTISFSLGKVSYLGTGEQYILKESQGGHDCISLGMGLDIPPPAGPLWILGVDF 376

QY 378 LGTYVAVFDRGDMKSSARVGLAR 403
DB 377 IGYTYTVFDR----ENNRVGFKA 398

RESULT 12
O93428 PRELIMINARY; PRT; 396 AA.
AC O93428
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cathepsin D precursor.
OS Chionodraco hamatus (Antarctic teleost icefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Nototheniidae; Channichthyidae; Chionodraco.
OX NCBI_TaxID=36188;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99227072; PubMed=10209280;
RA Capasso C., Lees W.E., Capasso A., Scudiero R., Carginali V.,
RA Kille P., Kay J., Parisi E.;
RT "Cathepsin D from the liver of the antarctic icefish Chionodraco
RT hamatus exhibits unusual activity and stability at high
RT temperatures.";
RL Biochim. Biophys. Acta 1431:64-73(1999).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR EMBL; AJ007878; CAA07719.1; -.
DR HSSP; P07339; 11YB.
DR MEROPS; A01.009; -.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001969; Asparticase AS.
DR InterPro; IPR001461; Peptidase A1.
DR InterPro; IPR009007; Pept_A_acid.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
DR Aspartyl protease; Hydrolase; Protease; Signal.
KW SIGNAL 1 18 POTENTIAL.
FT CHAIN 62 396 CATHEPSIN D.
SQ SEQUENCE 396 AA; 42662 MW; 62DAE23CCDF805A CRC64;

Query Match 44.0%; Score 985.5; DB 13; Length 396;
Best Local Similarity 47.7%; Pred. No. 7.3e-71;
Matches 195; Conservative 62; Mismatches 121; Indels 31; Gaps 5;

QY 10 LLLL-----LPLNVPSPGATLIRIPLH-----RVQGRRTINLLRGWREPAEL 53
DB 3 MLLLCVSALATINDAACSNSLKEIPFQTSADRLWEESRGAPRSLPEVQ-----LSF 57

QY 54 PKLGAPSGDKPIFVPLSNYRDVQYFGEIGLTPPQNTVAFDTGSSNLNVPVRRCHFFS 113
DB 58 PASNAPT-----ETLKNYLDQYGEIGLTPPQNTVAFDTGSSNLNVPVRRCHFFS 111

QY 114 VPCMLHRRFDPKASSFOANGTKPAIQTGTRVDGILSEDKLTGGIKGASVIFGEALWE 173
DB 112 IACLLHHKYSKGSSTVYKNGTAFATQIGSGLSGYLSQDTCTTGDAIADISQLFGEALQ 171

QY 174 PSLVFAFAHFGILGLGFPILSVEGVPPMDVLVEQLLDKPFVFLNRPDPDGGEL 233
DB 172 PGVAFIAKFGILGLGMAYPRISVDGVAFVFDNINSQKKVEKNVFSFLNRPDPDGGEL 231

QY 234 VLGGSDPAHYIPPIPTFVPVTPAYWQIHMERVKVGPGLTLCAGCAAILDTGSLITGPT 293
DB 232 LGGTDPKYYTGDYNDYDISQAYWQIRVDSMAVGDQLSLCTGCGEIVDSGTSITGPT 291

QY 294 BEIRALHAAIGIPLAGYIILCSEIPKLPVSLFLLGGVWNLTAHDYVIQTRNGVRL 353

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Db 359 MDIPPSG-LWTLGDVFGFYTVFDR-----ENDRVGLAKAK 395

RESULT 14

Q8J124 PRELIMINARY; PRT; 395 AA.

AC Q8J124;

DT 01-CCT-2002 (T-EMBLrel. 22, Created)

DT 01-CCT-2002 (T-EMBLrel. 22, Last sequence update)

DT 01-CCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Cathepsin D preproprotein.

OS Silurus asotus (Namazu) (Amur catfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

OC Siluridae; Silurus.

OX NCBI\_TaxID=30991;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21863985; PubMed=11821259;

RA Cho J.H., Park I.Y., Kim H.S., Lee W.T., Kim M.S., Kim S.C.;

RT "Cathepsin D produces antimicrobial peptide parasin I from histone H2A in the skin mucosa of fish.";

RL FASEB J. 16:429-431(2002);

DR EMBL; AF396662; AAM62283.1; -;

DR GO; GO:0004194; F:pepsin A activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR001969; Asparticase AS.

DR InterPro; IPR001461; Peptidase A1.

DR InterPro; IPR009007; Pept\_A\_acid.

DR Pfam; PF00026; asp; 1.

DR PRINTS; PR00792; PEPsin.

DR PROSITE; PS00141; ASP\_PROTEASE; 2.

SQ SEQUENCE 395 AA; 43030 MW; A731DBDE43664573 CRC64;

Query Match 43.5%; Score 974; DB 13; Length 395;

Best Local Similarity 48.3%; Pred. No. 6.1e-70;

Matches 195; Conservative 66; Mismatches 119; Indels 24; Gaps 6;

QY 10 LLLLLLLNVPESGATLIRPLHRVQGRRTIN-----LLRGWRPAELPKLG----- 57

Db 3 LACLLLVFIATADALVRIPLKFRSIRRTMSDSGRAVESRGNQTKY-ILGVTKNF 61

QY 58 APSGDKPIFVPLSNYRDVQYFGEIGLGTTPQNTFFVADTGSNNLWVPSRCHFSVPCW 117

Db 62 GTP-----ETLKNYLDQYVYGEIGLGTPTVQTTVFTDTSNNLWVPSVHCSTDIACL 115

QY 118 LHRFDPKASSSQFQANGKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEALWEPGLV 177

Db 116 LHKYNGAKSSTYVKNQAFALQYSGSLGSLGSDVCSIGDIAVEKQIFGEAIKQPGA 175

QY 178 FAFHFDGILGILGFPILSVGEVVRPMDVLVQGLDQKPVFSFYLNRPDEPDGGLVLGG 237

Db 176 FIAAKFDGLGMAYPRIADVGV-PVFDMMQSKKFNKVFVFLNRPDTPQGGELLGG 234

QY 238 SDPAHYIPLFVPTVYVAYQWQHMERVKVPGGLTCAKGAAILDTGTSLLTGTETIR 297

Db 235 TDPKFTYGDHYVNTTQAYQWQHMDGMSIGSLGCGGCAIVDTGTSLLTGTAAEVK 294

QY 298 ALHAAGGIPILAGVYIILCEIPKLPVAVSFLGGVWFNLTAHDYVVIOTTRNGVRLCLSG 357

Db 295 ALQKAIKAIPLIQGEVWDCKVPSLPISFNLGGQVTLTGEQYILKESQAGREICLSG 354

QY 358 FOALDVPVPPAGFWILGDVFLGTGYVAVFDRGDMKKSARVGLARA 401

Db 355 FVALDIPPPAGFWILGDVFLGTGYVAVFDRGDMKKSARVGLARA 401

RESULT 15

Q7Z1E4 PRELIMINARY; PRT; 385 AA.

AC Q7Z1E4;

DT 01-OCT-2003 (T-EMBLrel. 25, Created)

DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)

Db 292 VEVALQKALGAPFLIOGEYWNVCDTVPSLVSFTVGGQVYTLTGBOYILKVTQAGKTM 351

QY 354 CLSGFQALDVPVPPAGFWILGDVFLGTGYVAVFDRGDMKKSARVGLARAR 402

Db 352 CLSGFMGLDIPAPAGPLWILGDVFMQGYTVFDR-----DANRVGFAKAK 396

RESULT 13

Q9W6D4 PRELIMINARY; PRT; 397 AA.

AC Q9W6D4;

DT 01-NOV-1999 (T-EMBLrel. 12, Created)

DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Cathepsin D (EC 3.4.23.5).

OS Hynobius leechii (Korean salamander).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Cryptobranchioidea; Hynobiidae; Hynobius.

OX NCBI\_TaxID=113391;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20358712; PubMed=10902906;

RA Ju B.G., Kim W.S.;

RT "Cloning of a cDNA encoding cathepsin D from salamander, Hynobius leechii, and its expression in the limb regenerates.";

RL DNA Seq. 11:21-28(2000).

CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

DR EMBL; AF115925; AAD33219.1; -;

DR HSSP; P07339; 1LYB.

DR MEROPS; A01.009; -;

DR GO; GO:0004192; F:cathepsin D activity; IEA.

DR GO; GO:0004194; F:pepsin A activity; IEA.

DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR001969; Asparticase AS.

DR InterPro; IPR001461; Peptidase A1.

DR InterPro; IPR009007; Pept\_A\_acid.

DR Pfam; PF00026; asp; 1.

DR PRINTS; PR00792; PEPsin.

DR PROSITE; PS00141; ASP\_PROTEASE; 2.

KW Aspartyl protease; Hydrolase; Protease.

SQ SEQUENCE 397 AA; 42855 MW; 75CB1EA482D3DFE9 CRC64;

Query Match 43.7%; Score 977; DB 13; Length 397;

Best Local Similarity 48.3%; Pred. No. 3.5e-70;

Matches 194; Conservative 70; Mismatches 116; Indels 22; Gaps 5;

QY 10 LLLLLLLNVPESGATLIRPLHRVQGRRTINLLRGWRPAELPKLGAPSPGDKPIFVP 69

Db 7 LILLAPLLALHA--MVRPLTKFRSIRHTLTAEG-----DKNLVATSDQVKNYCP 58

QY 70 -----LSNYRDVQYFGEIGLGTTPQNTFFVADTGSNNLWVPSRCHFSVPCWLH 120

Db 59 KTQQTPELKNYLDQYVYGEIGLGTTPQNTFFVADTGSNNLWVPSVHCSTDIACLVRP 118

QY 121 RDPKASSSQFQANGKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEALWEPGLV 180

Db 119 KYDSSSSSTYVKNQAFALQYSGSLGSLGSLRQDTSVGGVLKQVFGAIPQGVAFIA 178

QY 181 AHFDGILGILGFPILSVGEVVRPMDVLVQGLDQKPVFSFYLNRPDEPDGGLVLGG 240

Db 179 AKFDGILGMAYPRIADVGV-PVFDMMQSKKFNKVFVFLNRPDTPRPGELLGGTDP 238

QY 241 AHYIPLFVPTVYVAYQWQHMERVKVPGGLTCAKGAAILDTGTSLLTGTETIRALH 300

Db 239 NYTGTFTYLNTPKAYQWQHMDGMSIGSLGCGGCAIVDTGTSLLTGTAAEVK 298

QY 301 AAGGGIPILAGVYIILCEIPKLPVAVSFLGGVWFNLTAHDYVVIOTTRNGVRLCLSGFOA 360

Db 299 KALGAIPLIOGEYWNVCDTVPSLVSFTVGGQVYTLTGBOYILKVTQAGKTM 358

QY 361 LDVPPVPPAGFWILGDVFLGTGYVAVFDRGDMKKSARVGLARAR 402



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:05:19 ; Search time 16.3371 seconds  
(without alignments)  
1338.637 Million cell updates/sec

Title: US-09-700-770-8

Perfect score: 2238

Sequence: 1 MSPPPPLQLPLLLLLLPLLNVE.....ARTRGADLGMGCTAQAQPPG 420

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2232	99.7	420	1	NAP1_HUMAN
2	1560.5	69.7	419	1	KDAP_MOUSE
3	1030	46.0	398	1	CATD_CHICK
4	1019.5	45.6	396	1	CATD_CLUHA
5	1015	45.4	412	1	CATD_HUMAN
6	1005	44.9	407	1	CATD_RAT
7	992.5	44.3	410	1	CATD_MOUSE
8	967.5	43.2	390	1	CATD_BOVIN
9	964.5	43.1	387	1	ASPP_AEDAE
10	944	42.2	345	1	CATD_PIG
11	922.5	41.2	365	1	CATD_SHEEP
12	878	39.2	397	1	CATE_MOUSE
13	869	38.8	396	1	CATE_HUMAN
14	867	38.7	398	1	CATE_RAT
15	848.5	37.9	396	1	CATE_RABIT
16	830	37.1	508	1	ASPR_HORVU
17	808.5	36.1	401	1	RENS_MOUSE
18	806.5	36.0	391	1	CATE_CAVPO
19	804	35.9	509	1	APR1_ORYSA
20	797	35.6	402	1	RENI_MOUSE
21	783	35.0	400	1	RENI_SHEEP
22	781	34.9	473	1	CYPL1_CYNCA
23	779	34.8	402	1	RENI_RAT
24	779	34.8	406	1	RENI_HUMAN
25	779	34.8	406	1	RENI_PANTR
26	773.5	34.6	496	1	ASPR_ORYSA
27	769.5	34.4	513	1	ASPR_CUCPE
28	767.5	34.3	388	1	PEP4_MACFU
29	765.5	34.2	388	1	PEP4_MACMU
30	759.5	33.9	388	1	PEP4_HUMAN
31	757.5	33.8	388	1	PEP2_MACFU
32	756	33.8	398	1	ASP3_CAEBL
33	755.5	33.8	388	1	PEP1_MACFU

34	735.5	32.9	386	1	PEPA_PIG
35	735	32.8	387	1	PEP2_RABIT
36	733	32.8	387	1	PEP4_RABIT
37	717	32.0	387	1	PEP1_RABIT
38	707.5	31.6	383	1	PEPE_CHICK
39	702	31.4	387	1	PEPA_CALJA
40	700	31.3	396	1	CARP_NEUCR
41	687.5	30.7	394	1	PEPC_CAVPO
42	685	30.6	387	1	PEP3_RABIT
43	685	30.6	405	1	CARP_YEAST
44	680.5	30.4	392	1	PEPC_RAT
45	679.5	30.4	381	1	CHYM_SHEEP

#### ALIGNMENTS

RESULT 1  
NAP1\_HUMAN  
ID NAP1\_HUMAN STANDARD; PRT; 420 AA.  
AC O96009;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Napsin 1 precursor (EC 3.4.23.-) (Napsin A) (NAPA) (TA01/TA02)  
DE (Aspartyl protease 4) (Asp 4) (ASP4).  
GN NAP1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney, and Lung;  
RX MEDLINE=95092989; PubMed=9877162;  
RA Tatnell P.J., Powell D.J., Hill J., Smith T.S., Tew D.G., Kay J.;  
RT "Napsins: new human aspartic proteinases. Distinction between two  
RT closely related genes.";  
RL FEBS Lett. 441:43-48(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Koeisch G., Wu S., Henthorn J., Tang J., Lin X.;  
RT "New human aspartic proteases napsin 1 and napsin 2: molecular  
RT cloning and intracellular localization of napsin 1.";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Fetal lung;  
RX MEDLINE=20047840; PubMed=10580105;  
RA Chuman Y., Bergman A.-C., Ueno T., Saito S., Sakaguchi K.,  
RA Alaya A.A., Franzen B., Bergman T., Arnott D., Auer G., Appella E.,  
RA Joernvall H., Linder S.;  
RT "Napsin A, a member of the aspartic protease family, is abundantly  
RT expressed in normal lung and kidney tissue and is expressed in lung  
RT adenocarcinomas.";  
RL FEBS Lett. 462:129-134(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Bienkowski M.J., Shuck M.E., Slightom J.L., Drong R.F.;  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: May be involved in processing of pneumocyte surfactant  
CC precursors.  
CC -!- TISSUE SPECIFICITY: Expressed predominantly in adult lung (type II  
CC pneumocytes) and kidney and in fetal lung. Low levels in adult  
CC spleen and very low levels in peripheral blood leukocytes.  
CC -!- SIMILARITY: Belongs to peptidase family A1.  
CC  
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CC EMBL; AF090386; AAD04917.1; -.
CC EMBL; AF098484; AAD13215.1; -.
CC EMBL; AF200345; AAF17081.1; -.
CC HSSP; P00797; 2REN.
CC MEROPS; A01.046; -.
CC MIM; 605631; -.
CC GO; GO:0004190; P:aspartic-type endopeptidase activity; TAS.
CC GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
CC InterPro; IPR001969; Aspartic-type endopeptidase AS.
CC InterPro; IPR009007; Peptidase A1.
CC InterPro; IPR001461; Peptidase A1.
CC Pfam; PF00026; asp; 1.
CC PRINTS; P00792; PPSIN.
CC PROSITE; PS00141; ASP_PROTEASE; 2.
CC KWL; Hydroxylase; Aspartyl protease; Glycoprotein; Zymogen; Signal.
CC FT SIGNAL 1 25 POTENTIAL.
CC FT PROPEP 26 63 ACTIVATION PEPTIDE.
CC FT CHAIN 64 420 NAPSIN 1.
CC FT ACT_SITE 96 96 BY SIMILARITY.
CC FT ACT_SITE 283 283 BY SIMILARITY.
CC FT DISULFID 109 116 BY SIMILARITY.
CC FT DISULFID 274 278 BY SIMILARITY.
CC FT DISULFID 317 354 BY SIMILARITY.
CC FT CARBOHYD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SQ SEQUENCE 420 AA; 45386 MW; 018B86AE5BDC865 CRC64;

Query Match 99.7%; Score 2232; DB 1; Length 420;
Best Local Similarity 99.8%; Pred. No. 2.7e-172; Indels 0; Gaps 0;
Matches 419; Conservative 0; Mismatches 1;

QY 1 MSPPPLQLPQLLLPLNVEPSGATLIRPLHRVQPGRTLNLRGWRPAPLPLKLGAPS 60
DB 1 MSPPPLQLPQLLLPLNVEPSGATLIRPLHRVQPGRTLNLRGWRPAPLPLKLGAPS 60

QY 61 PGDKPIFVLSNRDQVQFGEIGLTPPQNTQVAFDTGSNLSNLPVRRCHFFSVPCWLHH 120
DB 61 PGDKPIFVLSNRDQVQFGEIGLTPPQNTQVAFDTGSNLSNLPVRRCHFFSVPCWLHH 120

QY 121 RPEPKASSPQANGTFAIQYGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAF 180
DB 121 RPEPKASSPQANGTFAIQYGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAF 180

QY 181 AHFDGILGLGFPILSVEGVRPMDVLVEQGLLDKVPFSFYLNDRDPDPDGGELVLGSDP 240
DB 181 AHFDGILGLGFPILSVEGVRPMDVLVEQGLLDKVPFSFYLNDRDPDPDGGELVLGSDP 240

QY 241 AHVIPPFTFVTPVPAWQIHMERVKVGRGLTCAKCAALDTGTSLTGPTFEETRALH 300
DB 241 AHVIPPFTFVTPVPAWQIHMERVKVGRGLTCAKCAALDTGTSLTGPTFEETRALH 300

QY 301 AAGIGPILLAGEYILLCEIPKLPVAFSFLGGVWFLNTAHDYVIQTTTRNGVRLCLSGFOA 360
DB 301 AAGIGPILLAGEYILLCEIPKLPVAFSFLGGVWFLNTAHDYVIQTTTRNGVRLCLSGFOA 360

QY 361 LDVPPPPAGPFWILGDFVLGTYVAVFDGDMKSSARVGLARTRTGADLHGWTGAQPPG 420
DB 361 LDVPPPPAGPFWILGDFVLGTYVAVFDGDMKSSARVGLARTRTGADLHGWTGAQPPG 420

```

## RESULT 2

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KDAP MOUSE
ID KDAP_MOUSE STANDARD; PRT; 419 AA.
AC 009043;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE DE Kidney-derived aspartic protease-like protein precursor (EC 3.4.23.-)
DE (KDAP-1) (KAP) (Napsin).

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GN KDAP OR MAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RX MEDLINE=97165997; PubMed=9013890;
RA Mori K., Ogawa Y., Tamura N., Ebihara K., Aoki T., Muro S., Ozaki S.,
RA Tanaka I., Tashiro K., Nakao K.;
RA "Molecular cloning of a novel mouse aspartic protease-like protein
RT that is expressed abundantly in the kidney.";
RL FEBS Lett. 401:218-222(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=20534768; PubMed=11082205;
RA Tatnell P.J., Cook M., Peters C., Kay J.;
RA "Molecular organization, expression and chromosomal localization of
RT the mouse pronapsin gene.";
RL Eur. J. Biochem. 267:6921-6930(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshitsuki S., Carninci P., Prange C.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- TISSUE SPECIFICITY: Expressed at the highest levels in the kidney,
CC at a moderate level in the lung, and at low levels in the spleen
CC and adipose tissue.
CC -1- SIMILARITY: Belongs to peptidase family A1.
CC
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EMBL; D88899; BAA19004.1; -.
EMBL; AJ250718; CAB82907.1; -.
EMBL; AJ250719; CAB82907.1; JOINED.
EMBL; AJ250720; CAB82907.1; JOINED.
EMBL; BC014813; AAF14813.1; -.
HSSP; P00797; 2REN.
MEROPS; A01.046; -.
MGD; MGI:103365; Kdap.
InterPro; IPR001969; Aspartic-type AS.
InterPro; IPR009007; Peptidase A1.
InterPro; IPR001461; Peptidase A1.
Pfam; PF00026; asp; 1.
PRINTS; P00792; PPSIN.
PROSITE; PS00141; ASP_PROTEASE; 2.

```





RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Iqbalan N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McLean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzyzinski M.I., Skalska U.,  
RA Schnorch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
RN [5]  
RN SEQUENCE OF 1-22 FROM N.A.  
RP MEDLINE=94085791; PubMed=8262386;  
RX May F.E., Smith D.J., Westley B.R.;  
RA "The human cathepsin D-encoding gene is transcribed from an estrogen-  
RT regulated and a constitutive start point.";  
RL Gene 134:277-282(1993).  
RN [6]  
RN SEQUENCE OF 1-22 FROM N.A.  
RX MEDLINE=95021301; PubMed=7935485;  
RA Augereau P., Miralles F., Cavailles V., Gaudelet C., Parker M.,  
RA Rochefort H.;  
RA "Characterization of the proximal estrogen-responsive element of  
RT human cathepsin D gene.";  
RL Mol. Endocrinol. 8:693-703(1994).  
RN [7]  
RN SEQUENCE OF 170-180.  
RP TISSUE=Liver;  
RX Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,  
RA Appel R.D., Hughes G.J.;  
RL Submitted (JUN-1992) to Swiss-Prot.  
RN [8]  
RN CARBOHYDRATE-LINKAGE SITE ASN-263.  
RX MEDLINE=22660472; PubMed=12754519;  
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;  
RT "Identification and quantification of N-linked glycoproteins using  
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";  
RL Nat. Biotechnol. 21:660-666(2003).  
RN [9]  
RN VARIANT VAL-58.  
RX MEDLINE=20179010; PubMed=10716266;  
RA Papasotiropoulos A., Bagli M., Kurz A., Kornhuber J., Forstl H.,  
RA Majer W., Pauls J., Lautenschlager N., Heun R.;  
RT "A genetic variation of cathepsin D is a major risk factor for  
RT Alzheimer's disease.";  
RL Ann. Neurol. 47:399-403(2000).  
RN [10]  
RN X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).  
RP TISSUE=Spleen;  
RX MEDLINE=93223670; PubMed=8467789;  
RA Metcalf P., Fusek M.;  
RT "Two crystal structures for cathepsin D: the lysosomal targeting  
RT signal and active site.";  
RL EMBO J. 12:1293-1302(1993).  
RN [11]  
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RP TISSUE=Liver;  
RX MEDLINE=93342076; PubMed=8393577;  
RA Baldwin E.T., Bhat T.N., Gulnik S., Hosur M.V., Sowder R.C. II,  
RA Cachau R.E., Collins J., Silva A.M., Erickson J.W.;  
RT "Crystal structures of native and inhibited forms of human cathepsin  
RT D: implications for lysosomal targeting and drug design.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:6796-6800(1993).  
CC -!- FUNCTION: Acid protease active in intracellular protein breakdown.  
CC Involved in the pathogenesis of several diseases such as breast

CC cancer and possibly Alzheimer's disease.  
CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,  
CC that of pepsin A. Does not cleave the 4-Gln-His-5 bond in B  
CC chain of insulin.  
CC -!- SUBUNIT: Consists of a light chain and a heavy chain.  
CC -!- SUBCELLULAR LOCATION: Lysosomal.  
CC -!- POLYMORPHISM: The Val-58 allele is significantly overrepresented  
CC in demented patients (11.8%) compared with nondemented controls  
CC (4.9%). Carriers of the Val-58 allele have a 3.1-fold increased  
CC risk for developing AD than noncarriers.  
CC -!- SIMILARITY: Belongs to peptidase family A1.  
CC -----  
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CC -----  
CC EMBL; M1233; AAB59529.1; -;  
CC EMBL; X05344; CAA28955.1; -;  
CC EMBL; M63138; AAS1922.1; -;  
CC EMBL; M63134; AAS1922.1; JOINED.  
CC EMBL; M63135; AAS1922.1; JOINED.  
CC EMBL; M63136; AAS1922.1; JOINED.  
CC EMBL; M63137; AAS1922.1; JOINED.  
CC EMBL; BC016320; AAL16320.1; -;  
CC EMBL; L12980; AAL16314.1; -;  
CC EMBL; S74689; AAD14156.1; -;  
CC EMBL; S52557; AAD13868.1; -;  
CC PIR; A25771; KKHUO.  
CC PDB; 1LYA; 31-JAN-94.  
CC PDB; 1LYB; 31-JAN-94.  
CC PDB; 1LYW; 22-JUL-99.  
CC MEROPS; A01.009; -;  
CC SWISS-2DPAGE; P07339; HUMAN.  
CC Siera-2DPAGE; P07339; -;  
CC Genew; HGNC:2529; CTSD.  
CC MIM; 116840; -;  
CC GO; GO:0004192; F:cathepsin D activity; TAS.  
CC InterPro; IPR001969; Aspartate AS.  
CC InterPro; IPR009007; Pept A acid.  
CC InterPro; IPR001461; Peptidase\_A1.  
CC Pfam; PF00026; asp; 1.  
CC PRINTS; PR00792; PEPsin.  
CC PROSITE; PS00141; ASP\_PROTEASE; 2.  
CC Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Signal; Zymogen;  
CC Polymorphism; Alzheimer's disease; 3D-structure.  
CC SIGNAL 1 18  
CC PROPEP 19 64  
CC CHAIN 65 412  
CC CHAIN 65 161  
CC CHAIN 169 412  
CC ACT SITE 97 97  
CC ACT SITE 295 295  
CC DISULFID 91 160  
CC DISULFID 110 117  
CC DISULFID 286 290  
CC DISULFID 329 366  
CC CARBOHYD 134 134  
CC CARBOHYD 263 263  
CC VAR-ANT 58 58  
CC -----  
CC STRAND 67 74  
CC TURN 75 77  
CC STRAND 78 85  
CC TURN 86 89  
CC STRAND 90 97  
CC TURN 98 99  
CC STRAND 103 107

N-LINKED (GLCNAC. . .).  
N-LINKED (GLCNAC. . .).  
A -> V (ASSOCIATED WITH INCREASED RISK IN  
AD; POSSIBLY INFLUENCES SECRETION AND  
INTRACELLULAR MATURATION; dbSNP:17571).  
/FTid=VAR\_011621.

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FT TURN 108 109
FT TURN 112 113
FT HELIX 115 118
FT TURN 119 119
FT STRAND 123 123
FT HELIX 125 127
FT TURN 129 130
FT STRAND 132 141
FT STRAND 146 158
FT STRAND 172 184
FT HELIX 188 192
FT STRAND 197 200
FT HELIX 204 206
FT HELIX 208 210
FT HELIX 214 220
FT TURN 221 222
FT STRAND 228 233

Query Match 45.4%; Score 1015; DB 1; Length 412;
Best Local Similarity 46.9%; Pred. No. 2.6e-74;
Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;

QY 1 MSPPPLOPLLLPLLVNVEGATLIRIPHRVQPGRTNLLRGWR-----PAELP 54
DB 1 MQPSSLLPLALCLL-----AAPASA-LVRIPLHKFTSIRRTMSEVGSVEDLIAGKPVSKY 55
QY 55 KLGAPSPGDKPIFVPLSNRYDVQVFGELGTTPQNETVAFDTGSSNLWVPSRRCHFFSV 114
DB 56 SQAVPAVTEGPPIPEVLKYNDAQYGEIGTGPQCFTVVDVTGSSNLWVPSIRHCKLLDI 115
QY 115 PCWLHHRDPDKASSFQANGKFAIQYGTGRVDGILSEDKLTI-----GGIKGA 163
DB 116 ACWIHKYNSDKSSYVKNKGSFDTIHYGSGLSGLYSDTVSVPCQSASSALGGVKVE 175
QY 164 SVIFGEALWERSLVFAFHFDGILGFPILSVEGVRPMDVLVQGLDKPVSFYLR 223
DB 176 RQVFGAATKQGITFAAKFDGILGMAYPRISVNNVLFVFDNMQQLVDQNFISFYLSR 235
QY 224 DPEPDGELVLGSDPAHYIPLTFVPTVFPVYQIHWKVKVGFGLTCAKGCACALID 283
DB 236 DPDAQGELMLGGDSKYKYSGLSYLVNTRKAYQVLDQVEVAGSLTCKEGCEAIVD 295
QY 284 TGTSLITGTEIRALHAAGIGPILLAGIYIILCSIEIPKLPVAVSFLLGWVFNLFADHYV 343
DB 296 TGTSLMVGVDEVELQKAGVPLIQEYMPICEKVSFTLPAITLKGKGVKLSPEYDT 355
QY 344 IOTTNGVRLCLSGQALDVPVPPAGPFWILGVFTGTYYAVEDRGMKSSARVGLARA 401
DB 356 LKVSQAGKTLCLSGPFGMDIPPPSGPLWILGDFVFGYTYTFDR-----DNNRVGFAEA 409

RESULT 6
CATD RAT
ID CATD RAT STANDARD; PRT; 407 AA.
AC P24268;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cathepsin D precursor (EC 3.4.23.5).
GN CTSD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Pituitary;
RX MEDLINE=91057150; PubMed=2243802;
RA Birch N.P., Loh Y.P.;
RT "Cloning, sequence and expression of rat cathepsin D.";
RL Nucleic Acids Res. 18:6445-6445 (1990).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 65-74; 118-127 AND 165-174.

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RC TISSUE=Liver;
RX MEDLINE=91354249; PubMed=1883350;
RA Fujita H., Tanaka Y., Noguchi Y., Kono A., Himeno M., Kato K.;
RT "Isolation and sequencing of a cDNA clone encoding rat liver
RT lysosomal cathepsin D and the structure of three forms of mature
RT enzymes.";
RL Biochem. Biophys. Res. Commun. 179:190-196 (1991).
RN [3]
RP SEQUENCE OF 134-170.
RX MEDLINE=89034127; PubMed=3182800;
RA Yonezawa S., Takahashi T., Wang X., Wong R.N.S., Hartsuck J.A.,
RA Tang J.;
RT "Structures at the proteolytic processing region of cathepsin D.";
RL J. Biol. Chem. 263:16504-16511 (1988).
CC -1- FUNCTION: Acid protease active in intracellular protein breakdown.
CC -1- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
CC that of pepsin A. Does not cleave the 4-Gln-His-5 bond in B
CC chain of insulin.
CC -1- SUBUNIT: Occurs as a mixture of both a single chain form and two
CC types of two chain (light and heavy) forms.
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- SIMILARITY: Belongs to peptidase family A1.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; X54467; CAA38349.1; -.
DR PIR: S13111; KHRTD.
DR HSSP: P07339; 1LVB.
DR MEROPS: A01.009; -.
DR InterPro: IPR001969; Asprotease_AS.
DR InterPro: IPR009007; Pept_Acid.
DR InterPro: IPR001461; Peptidase_A1.
DR Pfam: PF00026; asp; 1.
DR PRINTS: PR00792; PEPIN.
DR PROSITE: PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal;
KW Lysosome.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 64 ACTIVATION PEPTIDE (POTENTIAL).
FT CHAIN 65 407 CATHEPSIN D.
FT CHAIN 65 164 CATHEPSIN D 12 kDa LIGHT CHAIN.
FT CHAIN 165 164 CATHEPSIN D 30 kDa HEAVY CHAIN.
FT CHAIN 65 117 CATHEPSIN D 9 kDa LIGHT CHAIN.
FT CHAIN 118 407 CATHEPSIN D 34 kDa HEAVY CHAIN.
FT ACT_SITE 97 97 BY SIMILARITY.
FT ACT_SITE 290 290 BY SIMILARITY.
FT DISULFID 91 160 BY SIMILARITY.
FT DISULFID 110 117 BY SIMILARITY.
FT DISULFID 281 285 BY SIMILARITY.
FT DISULFID 324 361 BY SIMILARITY.
FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 258 258 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 15 15 D -> A (IN REF. 2).
FT CONFLICT 163 163 D -> T (IN REF. 3).
FT CONFLICT 205 205 K -> N (IN REF. 2).
FT CONFLICT 262 262 K -> N (IN REF. 2).
SQ SEQUENCE 407 AA; 44680 MW; C423AD4104D95F84 CRC64;

Query Watch 44.9%; Score 1005; DB 1; Length 407;
Best Local Similarity 48.3%; Pred. No. 1.6e-73;
Matches 196; Conservative 68; Mismatches 124; Indels 18; Gaps 4;

QY 10 LLLLLPLLVNVEGATLIRIPHRVQPGRTNLLRGWR-----PAELPKLGAPSPGD 63
DB 7 LLLLLGLL--DASSSALLIRIPLRKFTSIRRTMTVEGGSVEDLILKGPITKYSSOSPRTK 64
QY 64 KPFIPLSNRYDVQVFGELGTTPQNETVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFD 123

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Db 65 EPVSELLKNYLDQAQYIGIGITPPQCFVTVDFTGSSNLWVPSHCKLLDIACVWHKYN 124
Qy 124 PKASSFOAGTCKAIOGTGRVDGILSED-----KLITGIGKASVIFGEALWEPGLV 177
Db 125 SDKSTVYKNGTSDIHVGSGLSGYSDQTVSVPCSKDGLGKVEKQIFGEATKQPGV 184
Qy 178 FAFHFDGILGLGFPILSVGEVRPMDVILVQGLLDKPVFVFLYLRNDPEEPDGGELVLGG 237
Db 185 FIAAFDGLGMPFFISVNVKVLVDFDNLKQKLVKKNIFSYLRNDPTGPGGELMLGG 244
Qy 238 SDPAHYTPPLTFVPTVPAYQIHMVRKVGPGGLTCLAKGCAALDTSITIGTTEIR 297
Db 245 TDSRYHGHLSYLVNTRKAYQVHMDOLEVSELTCLCKGGEALVDTGTSLLVGPVDEVK 304
Qy 298 ALHAAIGGIPILAGEYIILCEIPLKPAVSVLLGGVWENLTHDVIVCTTRNGVRLCLSG 357
Db 305 ELQKAIAGVLIQEQYMLPCBKVSLSPLITFKLGGQNVHELPEKVLKVSQAGKTICLSG 364
Qy 358 FQALDVPVPPAGPFWILGDFVLTGYVAVFDRGDMKSSARVGLARAT 403
Db 365 FMGMDIPPPGLWILGDFVLTGYVAVFDRGDMKSSARVGLARAT 406
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## RESULT 7

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CATD MOUSE STANDARD; PRT; 410 AA.
AC P18242;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cathepsin D precursor (EC 3.4.23.5).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=91088345; PubMed=2263503;
RA Diedrich J.F., Staakus K.A., Retzel E.F., Haase A.T.;
RT "Nucleotide sequence of a cDNA encoding mouse cathepsin D.";
RL Nucleic Acids Res. 18:7184-7184 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90326544; PubMed=2374732;
RA Grusby M.J., Mitchell S.C., Glimcher L.H.;
RT "Molecular Cloning of mouse cathepsin D.";
RL Nucleic Acids Res. 18:4008-4008 (1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=94280622; PubMed=8011168;
RA Hetman M., Perschl A., Saftig P., von Figura K., Peters C.;
RT "Mouse cathepsin D gene: molecular organization, characterization of
the promoter, and chromosomal localization.";
RL DNA Cell Biol. 13:419-427 (1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Acid protease active in intracellular protein breakdown.
CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
CC that of pepsin A. Does not cleave the 4-Gin-His-5 bond in B
CC chain of insulin.
CC -!- SUBUNIT: Consists of a light chain and a heavy chain.
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- SIMILARITY: Belongs to peptidase family A1.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; X53337; CAA37423.1; -
CC EMBL; X52886; CAA37067.1; -
CC EMBL; X68378; CAA48453.1; -
CC EMBL; X68379; CAA48453.1; JOINED.
CC EMBL; X68380; CAA48453.1; JOINED.
CC EMBL; X68381; CAA48453.1; JOINED.
CC EMBL; X68382; CAA48453.1; JOINED.
CC EMBL; X68383; CAA48453.1; JOINED.
CC EMBL; BC054758; AAH54758.1; -
CC EMBL; BC057931; AAH57931.1; -
CC PIR; I48278; KMSD.
CC HSP; P07339; ILYB.
CC MEROPS; A01.009; -.
CC MGD; MGI:88562; Ctad.
CC InterPro; IPR001969; Aspartate AS.
CC InterPro; IPR009007; Peptidase Al.
CC InterPro; IPR001461; Peptidase Al.
CC Pfam; PF00026; asp; 1.
CC PRINTS; PR00792; PEPSIN.
CC PROSITE; PS00141; ASP_PROTEASE; 2.
CC Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Zymogen; Signal.
CC SIGNAL 1 20 POTENTIAL.
CC PROPEP 21 64 ACTIVATION PEPTIDE (POTENTIAL).
CC CHAIN 65 410 CATHEPSIN D.
CC ACT_SITE 97 97 BY SIMILARITY.
CC DISULFID 91 160 BY SIMILARITY.
CC DISULFID 110 117 BY SIMILARITY.
CC DISULFID 284 288 BY SIMILARITY.
CC DISULFID 327 364 BY SIMILARITY.
CC CARBOHYD 134 134 N-LINKED (GLCNAC. .) (BY SIMILARITY).
CC CARBOHYD 261 261 N-LINKED (GLCNAC. .) (BY SIMILARITY).
CC SEQUENCE 410 AA; 44954 MW; DC4928EC46928BF0 CRC64;
Query Match 44.3%; Score 992.5; DB 1; Length 410;
Best Local Similarity 47.7%; Pred. No. 1.6e-72;
Matches 194; Conservative 67; Mismatches 125; Indels 21; Gaps 4;
Qy 10 LLLLLPLLVPEPGATLIRPLHRVQPGRTLLRGWRE-----PAELPKLGAPSPGD 63
Db 7 LLLLLGLL--ASSFAIRLIRPLKFTSIRKMTVGSGVEDLLKGPITKYSQSSPKTT 64
Qy 64 KPIFVPLSNRYDQYFGEIGLGTTPQNFTVAFTGSSNLWVPSRRCHFFSVPCWHLHRFD 123
Db 65 EPVSELLKNYLDQAQYIGIGITPPQCFVTVDFTGSSNLWVPSHCKLLDIACVWHKYN 124
Qy 124 PKASSFOAGTCKAIOGTGRVDGILSEDKLIT-----GGIGKASVIFGEALWEP 174
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Db 125 SSKSTVYKNGTSFDIHYGSGSLSGYLSDQTSVSPCKSQSKARGIKVEKQIFGEATKOP 184  
QY 175 SLVFAFAHEDGILGFGPILSVSGVRPPMDVLVEQGLDKPVFSFYINRDPEEPDGGELV 234  
Db 185 GIVEVAAREFDGILGWGPHISVNNVLPVFDNLMOQKLVKDNIFSFYINRDPEEPDGGELM 244  
QY 235 LGGSDPAHYPIPLTFVTVTPAYQIHMERYKVGPGTLCAKGCALIDTGTSLTGPTE 294  
Db 245 LGGTSKYHGLSVLNVTRKAYQVHMDQLEVGNELTCKGCEAIVDTGTSLVGPVE 304  
QY 295 EIRALHAAGTGGIPLAGEYIILCSEIPKLPVASFLLGGVWFNLTAHDYVVIQTRNGVRLC 354  
Db 305 EYKELQKALGAVFLIQEYIMPCERKSSLPVTYILKGGKNYELHPDKYILKVSQGGKTC 364  
QY 355 LSGFQALDVPVPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARA 401  
Db 365 LSGFGMDIPPPSGPLWILGDVFIGSYTVFDR----DNNRVGFANA 407

## RESULT 8

CATD\_BOVIN  
ID CATD\_BOVIN STANDARD; PRT; 390 AA.  
AC P80209; Q9TS27;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cathepsin D precursor (EC 3.4.23.5).  
OS CTSD.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP TISSUE=Milk;  
RC TISSUE=Milk;  
RX MEDLINE=93202276; PubMed=8454061;  
RA Larsen L.B., Boisen A., Petersen T.E.;  
RT "Procatepsin D cannot autoactivate to cathepsin D at acid pH.";  
RL FEBS Lett. 319:54-58(1993).  
RN [2]  
RC SEQUENCE OF 45-390, AND X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).  
RP TISSUE=Liver;  
RX MEDLINE=93223670; PubMed=8467789;  
RA Metcalf P., Fusek M.;  
RT "Two crystal structures for cathepsin D: the lysosomal targeting  
signal and active site.";  
RL EMBO J. 12:1293-1302(1993).  
CC -!- FUNCTION: Acid protease active in intracellular protein breakdown.  
CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,  
CC that of pepsin A. Does not cleave the 4-Gln-His-5 bond in B  
CC chain of insulin.  
CC -!- SUBUNIT: Consists of a light chain and a heavy chain.  
CC -!- SUBCELLULAR LOCATION: Lysosomal.  
CC -!- SIMILARITY: Belongs to peptidase family A1.  
DR HSP; P07339; 1LYB.  
DR MEROPS; A01.009; -.  
DR InterPro; IPR001969; Aspartic protease\_AS.  
DR InterPro; IPR009007; Pept\_Acid.  
DR InterPro; IPR001461; Peptidase\_A1.  
DR Pfam; PF00026; asp; 1.  
DR PRINTS; PR00792; PEPSIN.  
DR PROSITE; PS00141; ASP\_PROTEASE; 2.  
KW Hydroxylase; Aspartyl protease; Glycoprotein; Lysosome; Zymogen.  
FT PROPEP 1 44  
FT CHAIN 45 390  
FT ACT\_SITE 77 77  
FT ACT\_SITE 273 273  
FT DISULFID 71 140  
FT DISULFID 90 97  
FT DISULFID 264 268  
FT DISULFID 307 344  
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 390 AA; 42488 MW; 5B38AA1C33C48D35 CRC64;  
Query Match 43.2%; Score 967.5; DB 1; Length 390;  
Best Local Similarity 48.3%; Pred. No. 1.6e-70;  
Matches 189; Conservative 58; Mismatches 125; Indels 19; Gaps 3;  
QY 26 LIRIPLHRVQPPQRRNLRLRGW-----REPAELPKLGAPSPGDKPIFVPLSNYRDVQVF 79  
Db 1 VIRIPLHKFTSIRRTMSEAAGXVXXLIAKPIKSKYATGEPVAVRQGPIDELLKXNDAYY 60  
QY 80 GEIGLTGPQNPNTVAFDTGSSNLWVPSPRRCHFFSVPCWMLHHRFDPKASSFOANGTKPAI 139  
Db 61 GEIGLTGPQCPQTVVFDTGSAANLWVPSIHCILLDIACWTKRKYNSDKSSTVYKNGTTFDI 120  
QY 140 OYGTGRVDGILSEDKLT-----GKINGASVFECEALWEPSLVFAFAHEDGILG 190  
Db 121 HYGSGSLGYLSQDTVSPVPCNPSSSPGVTVQRTFGEARKQGVVFAIAKFDGILGMA 180  
QY 191 PFILSVGEVRPPMDVLVEQGLDKPVFSFYINRDPEEPDGGELVLGSDPAHYIPLTFV 250  
Db 181 YPRISVNNVLPVFDNLMOQKLVKDNVFSFELNROPKAPGGELMLGGTDSKYIRGSLMFH 240  
QY 251 PVTVPAYQIHMERYKVGPGTLCAKGCALIDTGTSLTGPTEIRALHAAIGIPLLA 310  
Db 241 NVTRQAYQIHMDDQLDVGSLSLTVCKGCEAIVDTGTSLVGPVEVRELOKAIGAVPLIQ 300  
QY 311 GEYIILCSEIPKLPVASFLLGGVWFNLTAHDYVVIQTRNGVRLCLSGFQALDVPVPGPF 370  
Db 301 GEYIMPCERKSSLPVTVKLGKDYALSPEDYALKVSOAETVCLSGFMGMDIPPPGGPL 360  
QY 371 WILGDVFLGTYVAVFDRGDMKSSARVGLARA 401  
Db 361 WILGDVFIGSYTVFDR----DNNRVGLAEA 387

## RESULT 9

ASPP\_AEDAE  
ID ASPP\_AEDAE STANDARD; PRT; 387 AA.  
AC Q03168;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lysosomal aspartic protease precursor (EC 3.4.23.-).  
OS Aedes aegypti (Yellowfever mosquito).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.  
OX NCBI\_TaxID=7159;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 54-71.  
RX MEDLINE=93016141; PubMed=1400492;  
RA Cho W.L., Raikhel A.S.;  
RT "Cloning of cDNA for mosquito lysosomal aspartic protease. Sequence  
analysis of an insect lysosomal enzyme similar to cathepsins D and  
E.";  
RL J. Biol. Chem. 267:21823-21829(1992).  
RN [2]  
RP CHARACTERIZATION.  
RA Cho W.-L., Dhadialla T.S., Raikhel A.S.;  
RT "Purification and characterization of a lysosomal aspartic protease  
with cathepsin D activity from the mosquito.";  
RL Insect Biochem. 21:165-176(1991).  
CC -!- FUNCTION: May degrade organelles involved in the biosynthesis and  
secretion of vitellogenin.  
CC -!- SUBUNIT: Homodimer.  
CC -!- SUBCELLULAR LOCATION: Lysosomal.  
CC -!- SIMILARITY: Belongs to peptidase family A1.  
CC  
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CC -----
CC EMBL; M95187; AAA29350.1; -.
DR PIR; A45117; A45117.
DR HSSP; P00797; 2REN.
DR MEROPS; A01.009; -.
DR Siena-2DPAGE; Q03168; -.
DR InterPro; IPR001969; Aspartate AS.
DR InterPro; IPR009007; Pept A acid_
DR InterPro; IPR001461; Peptidase_A1.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PRO0792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 18
FT PROPEP 19 53
FT CHAIN 54 387
FT ACT_SITE 86 86
FT ACT_SITE 272 272
FT DISULFID 99 106
FT DISULFID 263 267
FT DISULFID 306 343
FT CARBOHYD 123 123
SQ SEQUENCE 387 AA; 41805 MW; 73A3C9E701E47EEC CRC64;

Query Match 43.1%; Score 964.5; DB 1; Length 387;
Best Local Similarity 48.5%; Pred. No. 2.8e-70;
Matches 192; Conservative 62; Mismatches 131; Indels 11; Gaps 5;

QY 6 LLQPELLLLPLNVEPGATLIRPLHRVQGRRTLNLRGWRBFAELPKLGAPSPGDKP 65
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 2 LIKSIIALVCLAVL--SOADFRVQLHKTESARQHFRNVDTETIKQLRL-KYNAYS--GP 55

QY 66 IFVPLSNVRDQYGEIGLGPONFTVAFTGSSNLWVPSRRCHFFSVPCWLHHRFDPK 125
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 56 VPEPLSNYLDQYGAITGTPGSKVFDGSSNLWVPSKCSFTNACIMENKYNK 115

QY 126 ASSSFQANGTKFAIQYGTGRVDGLSEDKLIGIKGASVIFGEALWEPSPVFAFAFDG 185
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 116 KSTFFERKNGTAHFQYGGSGSLSVLSTDTVGLGGVSVTKQTFEAINEPGLVFAAFDG 175

QY 186 ILGLGFPLSVEGVRPMDVLVEQGLDKVPFSLNRPDPGEGELVGLGSPAHYIP 245
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 176 ILGLGYSISVDGVVPVFNFNQGLIDAPVFSYLNRPDPAEAGEGIIFGSDSNKYTG 235

QY 246 PLTFVPTVTPAYMOIHMERVKVPGGLTI-CAKGCRAILDTGSLITGPTTEIRALHAIGG 305
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 236 DFTYLSVDRKAYWQFMDSVKVG-DTEFCNNGCEALADTGTSLIAGPVSEVTAINKAIGG 294

QY 306 IPLLAGEYIILCSBIPKLPAPVSLFGVWVFNLTADHYVIQTRNGVRCLSGFQALDVP 365
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 295 TPIMNGEYMDCSLIPKLPKISFVLGKGSFLEAGDYVLRVAQNGKICLSGFMDIIPP 354

QY 366 PAGPFWILGDVFLTYVAVFDRGDMKSARVGLARA 401
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 355 PNGPLWILGDVFIKYYTEFDMG----NDRVGFATA 386
```

```
RESULT 10
CATD_PIG
ID CATD_PIG STANDARD; PRT; 345 AA.
AC P00795;
DT 21-JUL-1996 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cathepsin D (EC 3.4.23.5).
GN CTSD.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
```

```
RP SEQUENCE OF 1-98.
RC TISSUE=Spleen;
RX MEDLINE=83213348; PubMed=6406481;
RA Takahashi T., Tang J.;
RT "Am.no acid sequence of porcine cathepsin D light chain.";
RL J. Biol. Chem. 258:6435-6443(1983).
RN [2]
RP SEQUENCE OF 104-345.
RC TISSUE=Spleen;
RX MEDLINE=84222027; PubMed=6587385;
RA Shewale J.G., Tang J.;
RT "Am.no acid sequence of porcine spleen cathepsin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3703-3707(1984).
RN [3]
RP SEQUENCE OF 74-148 FROM N.A.
RX MEDLINE=89034127; PubMed=3182800;
RA Yonezawa S., Takahashi T., Wang X., Wong R.N.S., Hartsuck J.A.,
RT Tang J.;
RL "Structures at the proteolytic processing region of cathepsin D.";
RN [4]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=94152787; PubMed=642853;
RA Nakao Y., Kozutsumi Y., Kawasaki T., Yamashina I., van Halbeek H.,
RT Vliegenthart J.F.G.;
RL "Oligosaccharides on cathepsin D from porcine spleen.";
RN Arch. Biochem. Biophys. 229:43-54(1984).
CC -1- FUNCTION: Acid protease active in intracellular protein breakdown.
CC -1- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
CC that of pepsin A. Does not cleave the 4-Gln-His-5 bond in B
CC chain of insulin.
CC -1- SUBUNIT: Consists of a light chain and a heavy chain.
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- SIMILARITY: Belongs to peptidase family A1.
DR HSSP; P07339; ILVB.
DR MEROPS; A01.009; -.
DR InterPro; IPR001969; Aspartate AS.
DR InterPro; IPR009007; Pept A acid_
DR InterPro; IPR001461; Peptidase_A1.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PRO0792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Zymogen.
FT CHAIN 1 98
FT CHAIN 104 345
FT ACT_SITE 33 33
FT ACT_SITE 230 230
FT DISULFID 46 53
FT DISULFID 221 225
FT DISULFID 264 301
FT CARBOHYD 70 70
FT CARBOHYD 198 198
FT CARBOHYD 234 234
FT VARIANT 247 247
FT VARIANT 89 89
FT CONFLICT 97 97
FT CONFLICT C -> S (IN REF. 1).
SQ SEQUENCE 345 AA; 37295 MW; B3E72C11787F14E2 CRC64;

Query Match 42.2%; Score 944; DB 1; Length 345;
Best Local Similarity 52.7%; Pred. No. 1.1e-68;
Matches 183; Conservative 48; Mismatches 102; Indels 14; Gaps 4;

QY 65 PIFVPLSNVRDVOYFGEIGLGTTPQNTVAFTGSSNLWVPSRRCHFFSVPCWLHHRFDP 124
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 2 PIFVLKNYMDAQYGEIGLGTTPQNTVAFTGSSNLWVPSRRCHFFSVPCWLHHRFDP 61

QY 125 KASSSFQANGTKFAIQYGTGRVDGIL-SEDKLT-----ICGKASVIFGEALWEP 174
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 62 GKSTVYKNGTTFALHYGSGSLSGVLSQDTVSPCNLSALSGVGGIKVERQTGEATKQP 121

QY 175 SLVPAFAHFDGILGLGFPLSVEGVRPMDVLVEQGLDKVPFSLNRPDPGEGELV 234
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 122 GLTFIAAKFDGILGMAYPRISVNNVVFDFNLQKLVKDFSFYLNRPDPGAPGQGLM 181
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Qy 235 LGSDDPAHYIPPLTFVPTVYQWQHMERVKVGPGLTCAKGAAILDTGTSILITGTE 294
Db 182 LGGIDSKYKSLDYNHTRKAYQWQHNVAVGSSLTLCRGCEAIVDTGTSILVQPE 241
Qy 295 EIRALHAAGIPILLAGEYIILCSIEPKLPAVSLGGWGFNLTAHDVVIOTTRNGVRLC 354
Db 242 EVRELKALGAVFLIOGEMIPCEKVPSPDVTYTLGGKKYKLSSENVTAKVSGAQTC 301
Qy 355 LSGFQALDVPVPPAGFWLGVFLGTGYVAVFDRGDMKSSARVGLARA 401
Db 302 LSGFMGMDIPPPGGFLMGDFVIGRYTYTFDR-DLN---RVGLAEA 344

RESULT 11
CATD SHEEP
ID CATD SHEEP STANDARD; PRT; 365 AA.
AC Q9MZS8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cathepsin D precursor (EC 3.4.23.5) (fragment).
GN CTSD.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN 1;
RP SEQUENCE FROM N.A., AND VARIANT CONCL ASN-268.
RC STRAIN=White Swedish Landrace;
RX MEDLINE=20315862; PubMed=10856224;
RA Tyndela J., Sohar I., Sleat D.E., Gin R.M., Donnelly R.J., Baumann M.,
RA Halcia M., Lobel P.;
RT "A mutation in the ovine cathepsin D gene causes a congenital
RT lysosomal storage disease with profound neurodegeneration.";
RL EMBO J. 19:2786-2792(2000).
CC -!- FUNCTION: Cathepsin D is an acid protease active in intracellular
CC protein breakdown.
CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
CC that of pepsin A. Does not cleave the 4-Gln-|-His-5 bond in B
CC chain of insulin.
CC -!- SUBUNIT: Occurs as a mixture of both a single chain form and two
CC types of two chain (light and heavy) forms (By similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- DISEASE: Defects in CTSD are a cause of congenital ovine neuronal
CC ceroid lipofuscinosis (CONCL). CONCL is an autosomal recessive
CC disorder. Newborn lambs are weak, trembling, and unable to rise
CC and support their bodies. However, they are able to vocalize,
CC support their heads, and to suckle if bottle-fed. At autopsy, the
CC brains of affected lambs are strikingly small. The deep layers of
CC the cerebral cortex show pronounced neuronal loss, reactive
CC astrogliosis, and infiltration of macrophages. There is severe
CC degeneration of hippocampal pyramidal neurons.
CC -!- SIMILARITY: Belongs to peptidase family A1.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF164143; AAF80494.1; -.
CC HSSP; P07339; 1LYB.
CC MEROPS; A01.009; -.
CC InterPro; IPR001969; Aspartate AS.
CC InterPro; IPR009007; Peptidase A1.
CC InterPro; IPR001461; Peptidase_A1.
CC Pfam; PF00026; asp; 1.
CC PRINTS; PR00792; PEPSTN.
CC PROSITE; PS00141; ASP_PROTEASE; 2.
```

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KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen;
KW Lysosome; Disease mutation.
FT NON_TER 1
FT PROFEP <1 39 ACTIVATION PEPTIDE.
FT CHAIN 40 >365 CATHEPSIN D.
FT ACT_SITE 72 72 BY SIMILARITY.
FT ACT_SITE 268 268 BY SIMILARITY.
FT DISULFID 66 135 BY SIMILARITY.
FT DISULFID 85 92 BY SIMILARITY.
FT DISULFID 259 263 BY SIMILARITY.
FT DISULFID 302 339 BY SIMILARITY.
FT VARIANT 268 268 D -> N (IN CONCL; INACTIVE).
FT NON_TER 365
SQ SEQUENCE 365 AA; 39814 MW; 76A7BF5B5C45E9CB CRC64;

Query Match 41.2%; Score 922.5; DB 1; Length 365;
Best Local Similarity 47.7%; Pred. No. 6.2e-67;
Matches 175; Conservative 61; Mismatches 110; Indels 21; Gaps 4;

Qy 31 LHRVQPGRTLTLLRGLWREPAE-----LPKLGAPSPGDK--PIFVLSNYRDVQYFGE 81
Db 1 LHKFTSNRRITMSEAWG---PVEHLIAKGPISKYATREPAPVQGPPELLTNYMDAQYGE 57
Qy 82 IGLGTPQNFVAFDTGSSNLWVPSRRCHFFSPVCLHRRDPDKASSFQANGTKPAIQY 141
Db 58 IGIETPPQCFVWFDTGSAWLWVPSIHCKLDDIACWVHHKYNKSDKSTYVKNGTTFDIHY 117
Qy 142 GTGRVDGLTSEDKLT-----GGIKGASVFLGALWEPSSLVFAFAHFDGILGLGFP 192
Db 118 GSGSLGYLSQDTVSPVPCNPSSSPGGVTQVQRTGGEAIKQGVFFIAAKDGLGNMAYP 177
Qy 193 ILSVEGVRRPPMDVLVEQGLLDKPVFSFYLNRRDPPEPDGSELVLGGSDPAHYIPPLTFVY 252
Db 178 RISVNNVLPVDNLMRQKLVKDVNFSLNRRDPKRAQGEELMLG3TDSKYRGSILYHNV 237
Qy 253 TVPAWQIHMERVKVGPGTLTCAKGAAILDTGTSILITGPTTEIRALHAAGIPLAGE 312
Db 238 TRQAWQIHMQLDVGSLTVCCKGCEAIVDTGTSILWGPVDEVRLEHKAIGAVPLIQGE 297
Qy 313 YILCSIEPKLPAVSLGGWGFNLTAHDVVIOTTRNGVRLCISGFQALDVPVPPAGPWI 372
Db 298 YNIPCEKVSSLPQVTLKLGKDYTLSPEDYTLKVSQAGTTVCLSGFPMGMDIPPPGGPLMI 357
Qy 373 LGDVFGL 379
Db 358 LGDVFGL 364

RESULT 12
CATD MOUSE
ID CATD MOUSE STANDARD; PRT; 397 AA.
AC P70269; O35647;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cathepsin E precursor (EC 3.4.23.34).
GN CTSE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=Spleen;
RX MEDLINE=97324100; PubMed=9180269;
RA Tatnell P.J., Lees W.E., Kay J.;
RT "Cloning, expression and characterisation of murine procathepsin E.";
RL FEBS Lett. 408:62-66(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RA Tatnell P.J., Roth W., Duesing J., Kay J., Peters C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
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[3]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Due to its intracellular location and distribution in
CC lymphoid associated tissue, it may have a role in immune function.
CC -!- CATALYTIC ACTIVITY: Similar to cathepsin D, but slightly broader
CC specificity.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family A1.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL: X97399; CAA66056.1; -.
CC DR EMBL: Y10928; CAA71859.1; -.
CC DR EMBL: BC005432; AAH05432.1; -.
CC DR HSRF: P00794; 4CMS.
CC DR MEROPS: A01.010; -.
CC DR MGD: MGI:107361; Ctse.
CC DR InterPro: IPR001969; Aspprotease AS.
CC DR InterPro: IPR009007; Pept_Acid.
CC DR InterPro: IPR001461; Peptidase_A1.
CC DR Pfam: PF00026; asp; 1.
CC DR PRINTS: PR00792; PEPSIN.
CC DR PROSITE: PS00141; ASP_PROTEASE; 2.
CC KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal.
CC FT SIGNAL 1 18 BY SIMILARITY.
CC FT PROPEP 19 59 ACTIVATION PEPTIDE (BY SIMILARITY).
CC FT CHAIN 60 397 CATHEPSIN E.
CC FT ACT_SITE 97 97 BY SIMILARITY.
CC FT ACT_SITE 282 282 BY SIMILARITY.
CC FT DISULFID 61 61 INTERCHAIN (PROBABLE).
CC FT DISULFID 110 115 BY SIMILARITY.
CC FT DISULFID 273 277 BY SIMILARITY.
CC FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 323 323 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CONFLICT 297 297 H -> Q (IN REF. 2).
CC SQ SEQUENCE 397 AA; 42932 MW; 83993PFE3AB36105 CRC64;
Query Match 39.2%; Score 878; DB 1; Length 397;
Best Local Similarity 45.5%; Pred. No. 2.6e-63;
Matches 183; Conservative 67; Mismatches 138; Indels 14; Gaps 6;
OY 5 PLLQLLLLPLLVNPEPSGATLRIPLHRVQPGRTI-----NLRGWR-EPAELPKLGAP 59
Db 3 PLL--VLLLLLLLAQAGALHRVPLRLRHSRLKRGQAQQLSEFWRSHLDMTRLSES 60

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OY 60 SPGDKPIEVLPSNRDVOYFGEIGLGTPTTQFNTVAFDTGSSNLWVPSRRCHFFSVPCWLH 119
Db 61 CNVSSVNEPLINYLDMYFRTISIGTTPQNTVIFDGSNLMWVPSYVC--TSPACKAH 118
OY 120 HRDPKASSSQANGTKFAIQYGRVDGILSEDKLTIGGKIGKASVIFGEALWEPSLVFA 179
Db 119 PVFHPQSQDVTVEGNHFSIQYGTSLTGILGADQVSVEGLTVDGQQQFGESVKEPGQTFV 178
OY 180 FAHFDGILGLGFFPILSVEGVPPMDVLVEQGLLDKPVFYLNRDPEPDGDELVLGSD 239
Db 179 NAEFDGILGLGYSPLAAGGVTFVFDNMMAQNLVALPMFVSYLSSDPQGGSGSELTFFGYD 238
OY 240 PAHYIPPLTFVPVTPAYWQIHMVRKVPGLTLCAGKCAAILDTGSLITGPTTEIRAL 299
Db 239 PSFSGSLNWPVTKYQAWQIOLGIVQGVTFMFCSECCQAIQVDTGSLITGTPDKIKHL 298
OY 300 HAAFGIPLLAGEVYIILCSEIPKLPAYSVFLGGVWFLTAHYVIQYTRNGVRLCLGFG 359
Db 299 QEAICATP-IDGEYAVDCATLDTMENVTFILNVSYTLNPTDYILPLDVLDMGMQFCGSGFQ 357
OY 360 ALDVPPEPAGPPIILGDFVLTGYTVADEFGRGDKSSARVGLARA 401
Db 358 GLDIPPPAGPIIILGDFVFIQFYSFVDRG-----NNQVGLAPA 395
RESULT 14
CATE_HUMAN STANDARD; PRT; 396 AA.
AC P14091;
DT 01-JAN-1990 (Rel. 13, Created)
DT 10-JAN-1990 (Rel. 13, Last sequence update)
DE Cathepsin E precursor (EC 3.4.23.34).
GN CTSE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89380302; PubMed=2674141;
RA Azuma T., Pals G., Mohandas T.K., Couvreur J.M., Taggart R.T.;
RT "Human gastric cathepsin E. Predicted sequence, localization to
RT chromosome 1, and sequence homology with other aspartic
RT proteinases."
RL J. Biol. Chem. 264:16748-16753 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112877; PubMed=1370478;
RA Azuma T., Liu W.G., Vander Laan D.J., Bowcock A.M., Taggart R.T.;
RT "Human gastric cathepsin E gene. Multiple transcripts result from
RT alternative polyadenylation of the primary transcripts of a single
RT gene locus at 1q31-q32."
RL J. Biol. Chem. 267:1609-1614 (1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112877; PubMed=1370478;
RA Azuma T., Liu W.G., Vander Laan D.J., Bowcock A.M., Taggart R.T.;
RT "Human gastric cathepsin E gene. Multiple transcripts result from
RT alternative polyadenylation of the primary transcripts of a single
RT gene locus at 1q31-q32."
RL J. Biol. Chem. 267:1609-1614 (1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:14:10 ; Search time 28.59 Seconds  
(without alignments)  
1413.099 Million cell updates/sec

Title: US-09-700-770-8

Perfect score: 2238

Sequence: 1 MSPPPLLQPLLLPLLNVE.....ARTRGADLWGCTAQAPPG 420

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_78:\*  
1: Pirl1:\*  
2: Pirl2:\*  
3: Pirl3:\*  
4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1030	46.0	398	2	I51185
2	1015	45.4	412	1	KHHUD
3	1005	44.9	407	1	KHRTD
4	922.5	44.3	410	1	KHMSD
5	964.5	43.1	387	2	A45117
6	954.5	42.6	344	1	KHPGD
7	905.5	40.5	444	2	T24204
8	869	38.8	396	2	A34401
9	867	38.7	398	2	S66465
10	848.5	37.9	396	2	S36865
11	830	37.1	508	2	S19697
12	808.5	36.1	401	1	RMSS
13	806.5	36.0	391	2	A43356
14	804	35.9	509	2	S66516
15	803.5	35.9	442	2	JC5077
16	797	35.6	402	1	RMSK
17	789.5	35.3	365	2	S66466
18	783	35.0	400	2	I47099
19	779	34.8	402	1	RERTK
20	779	34.8	406	1	REHUK
21	778.5	34.8	474	2	T12049
22	778	34.8	513	2	T11686
23	774	34.6	506	2	T07915
24	774	34.6	508	2	D85056
25	773.5	34.6	496	2	U50732
26	769.5	34.4	513	2	T09739
27	767.5	34.3	388	1	S19682
28	766.5	34.2	506	2	F86253
29	765.5	34.2	388	1	PEMQAR

30 765.5 34.2 509 2 JC7272 aspartic proteinas  
31 765 34.2 506 2 S71591 aspartic proteinas  
32 760.5 34.0 428 2 S47096 cytarase (EC 3.4.2  
33 759.5 33.9 388 1 PEHU pepsin A (EC 3.4.2  
34 757.5 33.8 388 1 S19684 pepsin A (EC 3.4.2  
35 757.5 33.8 388 2 B30142 pepsin A (EC 3.4.2  
36 756 33.8 398 2 T33383 hypothetical prote  
37 755.5 33.8 388 1 PEMQAT pepsin A (EC 3.4.2  
38 754.5 33.7 388 2 A30142 pepsin A (EC 3.4.2  
39 754 33.7 509 2 S49349 cyprosin (EC 3.4.2  
40 737 32.9 387 2 C38302 pepsin (EC 3.4.23  
41 735.5 32.9 386 1 PRPG pepsin A (EC 3.4.2  
42 733 32.8 387 2 D38302 pepsin (EC 3.4.23  
43 717 32.0 385 2 JC7575 pepsinogen A bul  
44 717 32.0 387 2 B38302 pepsin (EC 3.4.23  
45 707.5 31.6 383 2 A41443 pepsin (EC 3.4.23

#### ALIGNMENTS

##### RESULT 1

I51185  
cathepsin D (EC 3.4.23.5) precursor - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 22-Jun-1999  
C:Accession: I51185  
R:Retzek, H.; Steyrer, E.; Sanders, E.J.; Nimf, J.; Schneider, W.J.  
DNA Cell Biol. 11, 661-672, 1992  
A:Title: Molecular cloning and functional characterization of chicken cathepsin D, a  
A:Reference number: I51185; MUID:93039672; PMID:1418623  
A:Accession: I51185  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-398 <RET>  
A:Cross-references: GB:S49650; NID:g259834; PIDN:AAB24157.1; PID:g259835  
C:Superfamily: pepsin  
C:Keywords: aspartic proteinase; hydrolase

Query Match 46.0%; Score 1030; DB 2; Length 398;  
Best Local Similarity 50.0%; Pred. No. 3.6e-78;  
Matches 208; Conservative 57; Mismatches 115; Indels 36; Gaps 7;

QY 1 MSPPPLLQPLLLPLLNVEPSGATLIRIPLRVQPGRRITLNLGRWREPAELPKGA-- 58  
DB 1 MAPRGLL--VLLLLAL--VGPC-AALIRIPITKFTSTRMLT-----EVGEIPDMNAIT 50  
QY 59 -----PSPGDKPIFVPLSNYRDVQYFGEIGLGTTPQNFPTAFDGTSSNLWV 104  
DB 51 QFLKFKLGADLAEPFP-----EILKNYMDAQYIGEIGTTPQKFTVVDGTSSNLWV 104  
QY 105 PSRCHFPSPVPCWLHHRFDPKASSFOANGTKPAIQVGTGRVDGILSEDKLTGCIKAS 164  
DB 105 PSVCHLLDACLHLHKYDASKSTYYENGTEFAIHYGTGSLGSLGSLQDTVTLLNLKKN 164  
QY 165 VIFGEALWEPSLVFAFAHFGIILGFPILSVGEVRPPMDVLEQGLDKPVPFYLNRD 224  
DB 165 QIFGEAVKQGIPTIAKFGIILGNAPRISVDKVTFFDNVMOQKLEKNIFSFLNRD 224  
QY 225 PEEPFGELVLGSDPAHYIPPLTFVPTVPAVQIHMERVKVPGPGLTLCAGCAAILDT 284  
DB 225 PTAQPGGELLGGTDPKYSGDFSWNVTRKAYQVHMSVDVANGLTLCCKGCEALVDT 284  
QY 285 GTSLLTGTPTREIRALHAIGIPLIAGEYIILCEIKPLPAVFLGGVFNLTAAHYVI 344  
DB 285 GTSLLTGTPTKEVKELOTAIGAKPLIKQYVISCDSKISLFPVTLMLGKPYQLTGEQYVF 344  
QY 345 QTTTANGVRLCLSGFOALDVPVPPAGPFWILGDVFLGTVAVFDRGDMKSSARVGLAR 400  
DB 345 KVSAGGETICLSGFSGLDVPVPPGGLMILGDVFLGTVAVFDR-----DNDSVGVPAK 396

##### RESULT 2



[illegible]



C:Superfamily: pepsin  
C:Keywords: aspartic proteinase; hydrolase; lysosome  
F:86,272/Active site: Asp #status predicted

Query Match 43.1%; Score 964.5; DB 2; Length 387;  
Best Local Similarity 48.5%; Pred. No. 16-72;  
Matches 192; Conservative 62; Mismatches 131; Indels 11; Gaps 5;

QY 6 LQPLLLPLINVPESGNTLIRPLHRVQPPRRINLLRWRPAAELPKLAPSGDKP 65  
DB 2 LKSIILVCLAVL--SQADFVRVQLHTESARQHRNVDTIKQLRL-KYNAVS---GP 55

QY 66 IFVPLSNRVDVQYFGEIGLGTGPQNTVAFDTGSSNLWVPSRRCHFFSVPCWLHRRDPK 125  
DB 56 VPEPLSNVLDQYGAITGTTPQSKVFDGSSNLWVPSKCEFTNIACLMKNYNAK 115

QY 126 ASSSQANGTKFAIQYGTGRVDGILSEDKLTITGGIKGASVIFGEALWPSLVFAFHFDG 185  
DB 116 KSTFEKNGTAFHIQYGGSSLSGYLSTDTVGLGGVSVTKQTFAEAINEPGLVFAAKFDG 175

QY 186 ILGLGFPILSVGVRPPMDVLVEQGLDKPVSFVNLNRPDPEPDGGLVGLGSDPAHYIP 245  
DB 176 ILGLGYSSLVGVVFPVFNMMQGLIDAPVFSFVNLNRPDPAEAGEIIFGGSNSKTYG 235

QY 246 PLTFVPTVPAYWQIHMERSVKVGPGLTLCAGCAAILDTGTSLITGPTTEIRALHAAIGG 305  
DB 236 DFTYLSVDRKAWQFKMDSVKVG-DTEFCNNGCEAIADTGTSLIAGPVSEVTAINKAIGG 294

QY 306 ILLAGEYIILGSEIPKLPVAVFLGGVFNLTADHYIQTTRNGVRLCLSGFQALDVPP 365  
DB 295 TPIMNGEYVMDCLPKLPKISFLVLGGKSFDLGADYVLRVAQMKGKTKICLSGFMGIDIPP 354

QY 366 PAGPFWILGDVFLGTYYAVFDRGDKMKSARVGLARA 401  
DB 355 ENGLPWILGDVFGIKYTFEDMG----NDRVGFAFA 386

RESULT 6  
KHPGD  
cathepsin D (EC 3.4.23.5) - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 18-Apr-1984 #sequence\_revision 31-Dec-1991 #text\_change 18-Mar-1997  
C:Accession: A93925; A93990; B31918; A00987  
R:Takahashi, T.; Tang, J.  
J. Biol. Chem. 258, 6435-6443, 1983  
A:Title: Amino acid sequence of porcine spleen cathepsin D light chain.  
A:Reference number: A92425; MUID:83213348; PMID:6406481  
A:Accession: A92425  
A:Molecule type: protein  
A:Residues: 1-95, 'S', 97 <TAK>  
A:Experimental source: spleen  
R:Shewale, J.G.; Tang, J.  
Proc. Natl. Acad. Sci. U.S.A. 81, 3703-3707, 1984  
A:Title: Amino acid sequence of porcine spleen cathepsin D.  
A:Reference number: A93990; MUID:84222027; PMID:6587385  
A:Accession: A93990  
A:Molecule type: protein  
A:Residues: 103-344 <SHE>  
A:Experimental source: spleen  
A:Note: 233-Lys and 246-Gln were also found  
R:Yonezawa, S.; Takahashi, T.; Wang, X.; Wong, R.N.S.; Hartsuck, J.A.; Tang, J.  
J. Biol. Chem. 263, 16504-16511, 1988  
A:Title: Structures at the proteolytic processing region of cathepsin D.  
A:Reference number: A92681; MUID:89034127; PMID:3182800  
A:Accession: B31918  
A:Molecule type: mRNA  
A:Residues: 74-146 <YON>  
A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. S6 in having an add  
C:Function:  
A:Description: limited specificity endopeptidase  
A:Pathway: intracellular protein degradation  
C:Superfamily: pepsin  
C:Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation

F:1-97/Product: cathepsin D light chain #status experimental <CDI>  
F:103-344/Product: cathepsin D heavy chain #status experimental <CDH>  
F:33,229/Active site: Asp #status experimental  
F:46-53,220-224,263-300/Disulfide bonds: #status predicted  
F:70,197/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:287/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 42.6%; Score 954.5; DB 1; Length 344;  
Best Local Similarity 52.9%; Pred. No. 5.9e-72;  
Matches 183; Conservative 48; Mismatches 102; Indels 13; Gaps 3;

QY 65 PIFPLSNRVDVQYFGEIGLGTGPQNTVAFDTGSSNLWVPSRRCHFFSVPCWLHRRDPK 124  
DB 2 PIPEVLKNYMDAQYGEIGLGTGPQNTVAFDTGSSNLWVPSRRCHFFSVPCWLHRRDPK 61

QY 125 KASSSQANGTKFAIQYGTGRVDGILSEDKLT-----IGGIKASVIFGEALWPS 175  
DB 62 GKSSTYVKNGTTFALHYGSSLSGYLSDTTSVPCNSALSAGVGKIKVERQTFGEATKPG 121

QY 176 LVFAFAHFDGILGLGFPILSVGVRPPMDVLVEQGLDKPVSFVNLNRPDPEPDGGLV 235  
DB 122 LTFIAAKFDGILGWAYPRISVNNVVPFDNIQQKLVKDIQFSLNRRDPGAQPGGELML 181

QY 236 GGSPPAHYIPPLTFVPTVPAYWQIHMERSVKVGPGLTLCAGCAAILDTGTSLITGPTTE 295  
DB 182 GGIDSKYKGLSDYHNTRKAYWQHNNQVAVGSSLTLCGCEAIADTGTSLIVGQPEE 241

QY 296 IRLHAAIGGIPLLAGEYIILGSEIPKLPVAVFLGGVFNLTADHYIQTTRNGVRLCL 355  
DB 242 VRELKATGAVELIQGEYMIPEKVPSPDVTITLGGKKYKLSSENYTLKVSQAGQTICL 301

QY 356 SGFQALDVPPAGPFWILGDVFLGTYYAVFDRGDKMKSARVGLARA 401  
DB 302 SGFMGDIPPPGGLWILGDVFGIKYTFEDR-DLN---RVGLARA 343

RESULT 7  
T24204  
hypothetical protein R12H7.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T24204  
R:Colles, L.  
submitted to the EMBL Data Library, August 1995  
A:Reference number: Z19854  
A:Accession: T24204  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-444 <WIL>  
A:Cross-references: EMBL:Z50755; PIDN:CAA90633.1; GSPDB:GNO0028; CESP:R12H7.2  
A:Experimental source: clone R12H7  
C:Genetics:  
A:Gene: CESP:R12H7.2  
A:Map position: X  
A:Introns: 29/2; 91/3; 133/1; 214/1; 395/2  
C:Superfamily: pepsin

Query Match 40.5%; Score 905.5; DB 2; Length 444;  
Best Local Similarity 49.7%; Pred. No. 1e-67;  
Matches 166; Conservative 58; Mismatches 105; Indels 5; Gaps 2;

QY 70 LSNRVDVQYFGEIGLGTGPQNTVAFDTGSSNLWVPSRRCHFFSVPCWLHRRDPK 129  
DB 86 LRYNDQYFTTISIGTPAQNTVFTDGSNLWIPSKCFYDIACMLHRRYDKSSST 145

QY 130 FOANGTKFAIQYGTGRVDGILSEDKLTITGGIKGASVIFGEALWPSLVFAFAHFDGILGL 189  
DB 146 KYEDGRKMAIQYGTGSMKGFISKDSVCAEDQPPAEATSPGITFVAAKFDGILGM 205

QY 190 GFFPLSVGVRPPMDVLVEQGLDKPVSFVNLNRPDPEPDGGLVGLGSDPAHYIPPLTF 249  
DB 206 AYPEAVILGVQVFNTLFEQKKVPSNLSFWLNRRNPSEIGETFFGIDISRRYVEPTY 265

QY 250 VPVTVPYQWQHMERKVGGLTLCRAKCAAILDTGTSILITGPTETRALHAAIGGIPLL 309  
 Db 266 VPVTRKGYWQFMDKV-VGSGVLCGNGCCAIADTGTSLIAGPKAQIEAIONFGRPEPLI 324  
 QY 310 AGRYIILCSIPKLPVAVSFLGGVWFLTAHDYVIOFTRNGVRLCUGSGFOALDVPPPPAG 369  
 Db 325 KGEYMTSCDKVPTLPVSVFVIGQEFSLKGEDYVVKVSGGKTKICLSGFMGIDLPRVGE 384  
 QY 370 FMIIGDVFELCTYAVEDRGDMKKSARVGLARAT 403  
 Db 385 LWILGDVFIKRYYSVFD----FDQNRVGFQAQAKT 414

RESULT 8  
 A34401  
 cathepsin E (EC 3.4.23.34) precursor - human  
 C/Species: Homo sapiens (man)  
 C/Date: 22-Jun-1990 #sequence revision 22-Jun-1990 #text\_change 22-Jun-1999  
 C/Accession: A42038; A34401; S35663; S34467; A34643; B34643  
 R/Azuma, T.; Liu, W.; Vander Laan, D.J.; Bowcock, A.M.; Taggart, R.T.  
 J. Biol. Chem. 267, 1609-1614, 1992  
 A/Title: Human gastric cathepsin E gene. Multiple transcripts result from alternative po  
 A/Reference number: A42038; MUID:92112877; PMID:1370478  
 A/Accession: A42038  
 A/Molecule type: DNA  
 A/Residues: 1-396 <AZU>  
 A/Cross-references: GB:M84424; GB:M82847; NID:g181203; PIDN:AAA52300.1; PID:g181205  
 A/Note: sequence extracted from NCBI backbone (NCBIN:75963, NCBIN:75966, NCBIN:75971, NC  
 R/Azuma, T.; Fale, G.; Mohandas, T.K.; Couvreur, J.M.; Taggart, R.T.  
 J. Biol. Chem. 264, 16748-16753, 1989  
 A/Title: Human gastric cathepsin E. Predicted sequence localization to chromosome 1, and  
 A/Reference number: A34401; MUID:89380302; PMID:2674141  
 A/Accession: A34401  
 A/Molecule type: mRNA  
 A/Residues: 1-396 <AZ2>  
 A/Cross-references: GB:J05036; NID:g181193; PIDN:AAA52130.1; PID:g181194  
 R/Takeda-Ezaki, M.; Yamamoto, K.  
 Arch. Biochem. Biophys. 304, 352-358, 1993  
 A/Title: Isolation and biochemical characterization of procathepsin E from human erythro  
 A/Reference number: S35663; MUID:93349047; PMID:8346912  
 A/Accession: S35663  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 20-38;54-76 <TAK>  
 R/Hill, J.; Montgomery, D.S.; Kay, J.  
 FEBS Lett. 326, 101-104, 1993  
 A/Title: Human cathepsin E produced in E. coli.  
 A/Reference number: S34467; MUID:93314762; PMID:8325357  
 A/Accession: S34467  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 57-60;62-81 <HIL>  
 R/Achouda, S.B.P.; Matsuzaki, O.; Kageyama, T.; Takahashi, K.  
 Biochem. Biophys. Res. Commun. 168, 878-885, 1990  
 A/Title: Structural evidence for two isozymic forms and the carbohydrate attachment site  
 A/Reference number: A34643; MUID:90241267; PMID:2334440  
 A/Accession: A34643  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 54-59, 'X', 61-68 <AT2>  
 C/Genetics:  
 A/Gene: GDB:CTSE  
 A/Map position: 1q31-1q31  
 A/Map position: 1q31-1q31  
 C/Superfamily: pepsin  
 C/Keywords: aspartic proteinase; blocked amino end; hydrolase; zymogen  
 F/1-17/Domain: signal sequence #status predicted <SIG>  
 F/18-53/Domain: activation peptide #status predicted <PRO>  
 F/54-396/Product: cathepsin E #status predicted <MAT>

F/18/Modified site: blocked amino end (Gln) (in mature form) (probably pyrrolidone ca  
 F/96,281/Active site: Asp #status predicted

Query Match 38.8%; Score 869; DB 2; Length 396;  
 Best Local Similarity 45.3%; Pred. No. 9.6e-65;  
 Matches 179; Conservative 70; Mismatches 136; Indels 12; Gaps 5;

QY 10 LLLLLLPLNVEPSGATLIRIPHRVQGRRTL-----NLLRGWR-EPAELPKLGAPSPGDK 64  
 Db 5 LLLLLLVLLEGEAQQSLHVRPLRRHPSLKKLRARSQSLSEFWKSHNLDMIQFTESCMDQ 64  
 QY 65 PIFVPLSNYRDVQYFGEIGLGTTPQNTFVADTGTSSNLNWPVSRCHFFSVPCWLHRRFDP 124  
 Db 65 SAKERPLNYLDMEYFGTISGSPQNTFVIFDTGSSNLNWPVSYVC--TSPACKTHERFQP 122  
 QY 125 KASSFQAGCTKFAIQYGTGRVDGILSEDKLTGGIKGASVIFGEALWEPVSLVFAAHD 184  
 Db 123 SQSTTYSQPGQSFIQIGTSLSGIIGADQVSGVEGTIVVQQQGESVTEPGQTIVDAEFD 182  
 QY 185 GILGLGFFILSVRGVPPMDVLVEQGLLDKVPFSFYINRDPEDPGGELVLGGSDFAHYI 244  
 Db 183 GILGLGYPVSLAVGVTFVFDNMAQNLVDLPMFESVTMSSNPEGAGSELIFGGYDHSFHS 242  
 QY 245 PPLTFVPTVPVAYWQHMERKVGPGGLTLCAGCAAILDTGTSILITGPTETRALHAAIG 304  
 Db 243 GSLNWPVPTKQAYWQIALDNIQVGTVMFCSEGCQAIQVDTGTSILITGSPDKIKOLQNAIG 302  
 QY 305 GIPLLAGEYIILCEIPKLPVAVSFLGGVWFLTAHDYVIOFTRNGVRLCUGSGFOALDV 364  
 Db 303 AAR-VGGEYAVECANLWMPDVTFTINGVPTLSPAYTLLDFVDMQFCSSGFGQLDIH 361  
 QY 365 PPAGPFWILGDVFLGTIVAVFDRGDMKKSARVGLARA 401  
 Db 362 PPAGPLWILGDVFIQYFVSFDRG-----NNRVGLAPA 394

RESULT 9  
 S66465  
 cathepsin E (EC 3.4.23.34) precursor (clone pTN05) - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 28-Oct-1996 #sequence revision 13-Mar-1997 #text\_change 20-Jun-2000  
 C/Accession: S66465; S74309  
 R/Okamoto, K.; Yu, H.; Misumi, Y.; Ikehara, Y.; Yamamoto, K.  
 Arch. Biochem. Biophys. 322, 103-111, 1995  
 A/Title: Isolation and sequencing of two cDNA clones encoding rat spleen cathepsin E  
 A/Reference number: S66465; MUID:96004785; PMID:7574663  
 A/Accession: S66465  
 A/Molecule type: mRNA  
 A/Residues: 1-398 <OKA>  
 A/Cross-references: EMBL:D45187; NID:g1113085; PIDN:BAA08128.1; PID:g1113086  
 A/Accession: S74309  
 A/Molecule type: protein  
 A/Residues: 20-47;59-91 <OKW>  
 C/Superfamily: pepsin  
 C/Keywords: aspartic proteinase; hydrolase  
 F/1-19/Domain: signal sequence #status predicted <SIG>  
 F/20-58/Domain: propeptide #status experimental <PRO>  
 F/59-398/Product: cathepsin E #status experimental <MAT>

Query Match 38.7%; Score 867; DB 2; Length 398;  
 Best Local Similarity 45.3%; Pred. No. 1.4e-64;  
 Matches 180; Conservative 68; Mismatches 137; Indels 12; Gaps 5;

QY 10 LLLLLLPLNVEPSGATLIRIPHRVQGRRTL-----NLLRGWR-EPAELPKLGAPSPGDK 64  
 Db 7 LLLLLLLDLAAQGVHLHVRPLRRHQSRLKRLKLAQQLSDFWKSHNLDMEFSESCNVDX 66  
 QY 65 PIFVPLSNYRDVQYFGEIGLGTTPQNTFVADTGTSSNLNWPVSRCHFFSVPCWLHRRFDP 124  
 Db 67 GINEPLNYLDMEYFGTISGSPQNTFVIFDTGSSNLNWPVSYVC--TSPACKAHPVFP 124  
 QY 125 KASSFQAGCTKFAIQYGTGRVDGILSEDKLTGGIKGASVIFGEALWEPVSLVFAAHD 184

```
Db 125 SOSSTYNEVGNHPSIOYGTGSLTGIIGADQVSVREGLTVEGQFCGESVKEPQQTFFVNAED 184
Qy 185 GILGLGFPILLSVGRVPMQVLEQGLLDKVPFVFNRPDEPDGGLVGLGSDPAHYI 244
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 185 GILGLGFPILLSVGRVPMQVLEQGLLDKVPFVFNRPDEPDGGLVGLGSDPAHYI 244
Qy 245 PPLTFVPTVPYAWQIHMWRVKVPGFGLTCAKGAAILDTGTSITGTEIRALHAAG 304
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 245 GSLNWPVTKGYWQIALDGTQVDTWFCSEGCQAIVDTGTSITGTPPKIKQLQEAIG 304
Qy 305 GIPLLAGYIILCEIPKLPVAVSFLGQVFNLTADHYVIOITRNGVRLCLSGFQALDVP 364
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 305 ATP-MDGEYAVDCATLNNMPNVTFLINGSVTLTPTAYILPDLVDGMQFCGSGFGGLDIQ 363
Qy 365 PPAGPFWILGVFLGTYYAVFDRGDMKSSARVGLARA 401
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 364 PPAGPFWILGVFLGTYYAVFDRGDMKSSARVGLARA 401

RESULT 10
S36865
cathepsin E (EC 3.4.23.34) precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 22-Jun-1999
C:Accession: S36865
R:Kageyama, T.
Eur. J. Biochem. 216, 717-728, 1993
A:Title: Rabbit procathepsin E and cathepsin E. Nucleotide sequence of cDNA, hydrolytic
A:Reference number: S36865; MUID:94009032; PMID:8404890
A:Accession: S36865
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-396 <KAG>
A:Cross-references: GB:L08418; MID:g402728; PIDN:AAC37308.1; PID:g402729
C:Superfamily: pepsin
C:Keywords: aspartic proteinase; hydrolase

Query Match 37.9%; Score 848.5; DB 2; Length 396;
Best Local Similarity 44.9%; Pred. No. 5e-63;
Matches 179; Conservative 68; Mismatches 137; Indels 15; Gaps 7;
Qy 9 PLLLLPLLNVPFSGATLIRIPHRVQPGRTNLNLRG-----WR-EPABLPKLGAPSPG 62
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 5 PLLALL-LLDLQAQCTLLDRVPLRR-OPSLRKKLAQAGQLSEFMAKHKVDMVQYTTCTM 62
Qy 63 DXPIFVPLSNYRDVQYFGEIGLGTDPQNETVAFDTGSSNLWVPSRCHFFSVPCWLHHRF 122
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 63 EQSANEPNLNLDMEYFGTISGSPQNPFTVFDTVSSNLWVPSVVC--TSPACOMHPQF 120
Qy 123 DPKASSFQANGTKFAIQYGTGRVDGILSEDKLTIGIKGASVIFGEALWEPSLVFAFAH 182
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 121 RPSQNTYSEVGTFFPSIAVTGSLTGIAGDQVSVQGLTVVGGQFGESVKEPQQTFFVNAE 180
Qy 183 FPGILGLGFPILLSVGRVPMQVLEQGLLDKVPFVFNRPDEPDGGLVGLGSDPAH 242
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 181 FPGILGLGFPILLSVGRVPMQVLEQGLLDKVPFVFNRPDEPDGGLVGLGSDPAH 240
Qy 243 YTPPLTFVPTVPYAWQIHMWRVKVPGFGLTCAKGAAILDTGTSITGTEIRALHAAG 302
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 241 FGSLSLWNPVTKGYWQIALDGTQVDTWFCSEGCQAIVDTGTSITGTPPKIKQLQEAIG 300
Qy 303 IGCIPLLAGYIILCEIPKLPVAVSFLGQVFNLTADHYVIOITRNGVRLCLSGFQALD 362
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 301 IGATP-MDGEYAVDCATLNNMPNVTFLINGSVTLTPTAYILPDLVDGMQFCGSGFGGLD 359
Qy 363 VPPAGPFWILGVFLGTYYAVFDRGDMKSSARVGLARA 401
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 360 IQPPAGPFWILGVFLGTYYAVFDRGDMKSSARVGLARA 394

RESULT 11
S19697
aspartic proteinase (EC 3.4.23.-) precursor - barley
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```
C:Species: Hordeum vulgare (barley)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999
C:Accession: S19697
R:Runeberg-Roos, P.; Toermeakangas, K.; Oestman, A.
Eur. J. Biochem. 202, 1021-1027, 1991
A:Title: Primary structure of a barley-grain aspartic proteinase. A plant aspartic pr
A:Reference number: S19697; MUID:92111473; PMID:1722454
A:Accession: S19697
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-508 <RUN>
A:Cross-references: EMBL:X56136; MID:g18903; PIDN:CAA39602.1; PID:g18904
C:Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent
C:Superfamily: oryzasin; saposin repeat homology
C:Keywords: aspartic proteinase; hydrolase
E:315-360/Domain: saposin repeat homology #status atypical <SAP1>
E:369-419/Domain: saposin repeat homology #status atypical <SAP2>
F:102,289/Active site: Asp #status predicted

Query Match 37.1%; Score 830; DB 2; Length 508;
Best Local Similarity 36.7%; Pred. No. 2.4e-61;
Matches 186; Conservative 54; Mismatches 147; Indels 120; Gaps 7;
Qy 6 LLQPLILLPLLNVPFSGATLIRIPHRVQPGRTNLNLRGWRPAPLKLGAESP-----61
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 10 LLAVALLLQTVLPAASEAGLVRLAKK-RPIDRNSRVATGLSGGEEQPLLSGANPLRSE 68
Qy 62 --GDKPIFVPLSNYRDVQYFGEIGLGTDPQNETVAFDTGSSNLWVPSRCHFFSVPCWLH 119
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 69 EEGD---IVALKNYNNQAYFGEIGVGPQKFTVIFDTGSSNLWVPSAKC-YPSIACVLH 124
Qy 120 HRFDPKASSFQANGTKFAIQYGTGRVDGILSEDKLTIGIKGASVIFGEALWEPSLVFA 179
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 125 SRYKAGASSTYKNGKPAAIQYGTGSIAGYSEDSVTVDLVVKDQBFIEATKEPGITFL 184
Qy 180 FAHFDGILGLGFPILLSVGRVPMQVLEQGLLDKVPFVFNRPDEPDGGLVGLGSD 239
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 185 VAKFDGILGLGFPILLSVGRVPMQVLEQGLLDKVPFVFNRPDEPDGGLVGLGSD 244
Qy 240 PAHYIPPLTFVPTVPYAWQIHMWRVKVPGFGLT-LCAKGAAILDTGTSITGTEIRA 298
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 245 PKHVGEITYVPTQKGYWQFDMGDVVGKSTGTCAGCAAIADSGTSLLAGPTALITE 304
Qy 299 LHAAIGG-----305
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 305 INEKIGAAGVWSQECTIVSQYQQLLDLLAETQPKKICQVGLCTPDGTRGVSAGIRS 364
Qy 306 -----IPLIAGEYI 314
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 365 VVDEPVSNGSLRADPMCSACEMAVVMQNQLAQNKTODLILDYVNLNRLPSPWGESA 424
Qy 315 ILCEIPKLPVAVSFLGQVFNLTADHYVIOITRNGVRLCLSGFQALDVPVPPAGPFWILG 374
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 425 VDCGSLGSMPEDEFTIGGKFKALKPEEYILKVGEGAAAQICISGTAMDIPPRGRLWIIG 484
Qy 375 DVFLGTYYAVFDRGDMKSSARVGLARA 401
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 485 DVFMGPYHTVFDYDKL-----RIGFAKA 507

RESULT 12
REMS
renin (EC 3.4.23.15) precursor, submandibular - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Oct-1982 #sequence_revision 17-Dec-1982 #text_change 18-Jun-1999
C:Accession: A93923; A93285; B93285; B22058; A00988
R:Wison, K.S.; Chang, J.J.; Inagami, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 4858-4862, 1982
A:Title: Amino acid sequence of mouse submaxillary gland renin.
A:Reference number: A93923; MUID:83014991; PMID:6812055
A:Accession: A93923
A:Molecule type: protein
A:Residues: 64-351;354-401 <MTS>
```

R:Panther, J.J.; Foote, S.; Chambrud, B.; Strosberg, A.D.; Corvol, P.; Rougeon, F.  
 Nature 298, 90-92, 1982  
 A:Title: Complete amino acid sequence and maturation of the mouse submaxillary gland renin  
 A:Reference number: A93285; MUID:82220074; PMID:6283373  
 A:Accession: A93285  
 A:Molecule type: mRNA  
 A:Residues: 1-36, 'M', 100-194, 'LSRS', 199-394, 'V', 396-401 <PAL>  
 A:Cross-references: GB:J00621; GB:V00845; NID:g200701; PIDN:AAA40050.1; PID:g200702  
 A:Note: The authors translated codon ATG for residue 99 as Ile  
 A:Accession: B93285  
 A:Molecule type: protein  
 A:Residues: 64-84; 354-374 <PA2>  
 R:Poe, M.; Liesch, J.M.  
 J. Biol. Chem. 258, 9856-9860, 1983  
 A:Title: Mouse submaxillary gland renin contains a noncovalently attached fatty acid.  
 A:Reference number: A92439; MUID:83290909; PMID:6350284  
 A:Contents: annotation; fatty acid binding  
 R:Panther, J.J.; Dreyfus, M.; Roux, D.T.L.; Rougeon, F.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 5489-5493, 1984  
 A:Title: Mouse kidney and submaxillary gland renin genes differ in their 5' putative region  
 A:Reference number: A22058; MUID:84298161; PMID:6089205  
 A:Accession: B22058  
 A:Molecule type: DNA  
 A:Residues: 1-29 <PAN>  
 C:Comment: The enzyme contains a noncovalently attached fatty acid.  
 C:Comment: Submandibular renin has catalytic and antigenic activities similar to renal renin  
 C:Comment: This renin is synthesized in the submandibular gland of males only.  
 C:Genetics:  
 A:Gene: REN2

C:Superfamily: pepsin  
 C:Keywords: aspartic proteinase; hydrolase; salivary gland; submandibular gland  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-63/Domain: activation peptide #status predicted <ACP>  
 F:64-351/Product: renin, submandibular, heavy chain #status experimental <RSH>  
 F:354-401/Product: renin, submandibular, light chain #status experimental <RSL>  
 F:101,286/Active site: Asp #status experimental  
 F:114-121,277-281,320-357/Disulfide bonds: #status predicted

Query Match 36.1%; Score 808.5; DB 1; Length 401;  
 Best Local Similarity 41.7%; Pred. No. 1.1e-59;  
 Matches 172; Conservative 62; Mismatches 147; Indels 31; Gaps 7;  
 QY 5 PLLOQLLLLLNVPESGATLIRIPHRVQPGRTLLNLRGWRPAPLKLGPAP----- 59  
 Db 7 PLWALLLLWSPCTSLPTGTTFTRIPKKM-PSVREILEERG----VDMTSLAEWDVFT 61  
 QY 60 -----SPGDKPIFVPLSNYRDVQYFGEIGLCTPPQNFVAFDTGSSNLWVPSRCH 110  
 Db 62 KRSLTDLISP-----VLTNYLNSQYIGEIGTPTPKVIFDTGSANLWVPSKCS 115  
 QY 111 FFSVPCWLHHRFDPKASSSFGANGTKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEA 170  
 Db 116 RLXLACGIHSLYESDSSSYEMENGDDFTHYGSRGVKFLSQDSVTVGGIT-VTQTFGEV 174  
 QY 171 LWESLVAFAHFDGILGEPILLSVEGRVPMQVLEQGLDKPVSFYLNRPDEPDG 230  
 Db 175 TELPLIPMLAQFDGVLGMGPPAQAVGVTFVDFHLSQGLKKEKVFVSYNRPGLL-G 233  
 QY 231 GELVLGGSDPAHYTPPLTFVTPVYQIHMVRKVGPGTLCAKGAAILDTGTSIT 290  
 Db 234 GEVLVGGSDPEHYQDGFHYVLSKTDSSQIITMKVSGVSSSTLLCEGCEGVVDVTSGPSIS 293  
 QY 291 GPTFEIRALHAAGIGPIPLAGEYIILCSEIKPLPAVSFLLGQVWFMNLTFAHDYVIQTTNRG 350  
 Db 294 APTSSLKIMQALGAKERHLYVVCVQVPLTLPDISFNLGGRATVLSSTDYVLYQPNR 353  
 QY 351 VRLCLSGQALDVPVPPAGFFILGVTYVAFVDFRGMKSSARVGLAR 402  
 Db 354 DKLCTVALHAMDIPPTGPFVVLGATFIRKFTYTFDR----HNNRIGFALAR 401

RESULT 13  
 A43356

cathepsin E (EC 3.4.23.34) precursor - guinea pig  
 N:Alternate names: erythrocyte membrane aspartic proteinase; slow-moving proteinase  
 C:Species: Cavia porcellus (guinea pig)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 22-Jun-1999  
 R:Kageyama, T.; Ichinose, M.; Takada, S.; Miki, K.; Kurokawa, K.; Koizumi, O.; Tanji  
 J. Biol. Chem. 267, 16450-16459, 1992  
 A:Title: Gastric procathepsin E and progastricsin from guinea pig. Purification, mol.  
 A:Reference number: A43356; MUID:92355614; PMID:1644829  
 A:Accession: A43356  
 A:Molecule type: mRNA  
 A:Residues: 1-391 <KAG>  
 A:Cross-references: GB:M88653; NID:g191294; PIDN:AAA37052.1; PID:g191295  
 A:Note: sequence extracted from NCBI backbone (NCBIN:110763, NCBI:110769)  
 C:Superfamily: pepsin  
 C:Keywords: aspartic proteinase; hydrolase; membrane protein

Query Match 36.0%; Score 806.5; DB 2; Length 391;  
 Best Local Similarity 42.8%; Pred. No. 1.6e-59;  
 Matches 170; Conservative 72; Mismatches 138; Indels 17; Gaps 7;  
 QY 10 LLLLLPLLNVPESGATLIRIPHRVQPGRTLLNLRGWRPAPLKLGPAPSGDK 64  
 Db 5 LLLLLLLELQAPCALHRVPLSRSLRKLKRAQGLTELKSNLMDQCSTIQSANE 64  
 QY 65 PIFVPLSNYRDVQYFGEIGLCTPPQNFVAFDTGSSNLWVPSRCHPFSVPCWLHHRFDP 124  
 Db 65 ---PLNLYLMEVFGIISGSPQNFVAFDTGSSNLWVPSVVC--TSPACQTHPVHP 118  
 QY 125 KASSSFGANGTKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEALMEPSLVAFAHFD 184  
 Db 119 SLSSTYREVGNFSIQYGTSLTGLIGADQVSEGLTVGQGGESVQEPKGTFFVHAEFD 178  
 QY 185 GILGLGEPILLSVEGRVPMQVLEQGLDKPVSFYLNRPDEPDGSELVLCGSDPAHYI 244  
 Db 179 GILGLGEPILLSVEGRVPMQVLEQGLDKPVSFYLNRPDEPDGSELVLCGSDPAHYI 237  
 QY 245 PPLTFVTPVYQIHMVRKVGPGTLCAKGAAILDTGTSITGTEIRALHAAG 304  
 Db 238 GSLNWPVTRQAYWQIALDGLQVDSVWFCEGQAIQVDTGTSITGTPPGKIKQLQALG 297  
 QY 305 GIPLLAGYIILCSEIKPLPAVSFLLGQVWFMNLTFAHDYVIQTTNRGVLCLSGFQALDVP 364  
 Db 298 ATYYDEG-YSVQCANLNMMLDVTIINGVPTLNTPTATLLDFVDGMQVCSGTEGLEIQ 356  
 QY 365 PPAGFFILGVTYVAFVDFRGMKSSARVGLAR 401  
 Db 357 PPAGFFILGVTYVAFVDFRGMKSSARVGLAR 389

RESULT 14  
 S66516  
 oryzasin (EC 3.4.23.-) precursor - rice  
 N:Alternate names: aspartic proteinase 1  
 C:Species: Oryza sativa (rice)  
 C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
 R:Asakura, T.; Watanabe, H.; Abe, K.; Arai, S.  
 Eur. J. Biochem. 232, 77-83, 1995  
 A:Title: Rice aspartic proteinase, oryzasin, expressed during seed ripening and germi  
 A:Reference number: S66516; MUID:96048031; PMID:7556174  
 A:Accession: S66516  
 A:Molecule type: DNA  
 A:Residues: 1-509 <ASA>  
 A:Cross-references: EMBL:D32165; NID:g511665; PIDN:BAA06876.1; PID:g1030715  
 A:Accession: S66517  
 A:Molecule type: mRNA  
 A:Residues: 1-509 <ASZ>  
 A:Cross-references: EMBL:D32144; NID:g1255684; PIDN:BAA06875.1; PID:g1711289  
 C:Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent  
 C:Genetics:  
 A:Introns: 119/3; 140/1; 171/3; 209/2; 265/3; 279/1; 300/3; 338/3; 360/2; 412/3; 452/  
 C:Superfamily: oryzasin; saposin repeat homology

C;Keywords: aspartic proteinase; hydrolase  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-68/Domain: propeptide #status predicted <PRO>  
F;68-509/Product: aspartic proteinase 1 #status predicted <MAT>  
F;316-361/Domain: saposin repeat homology #status atypical <SAP1>  
F;370-420/Domain: saposin repeat homology #status atypical <SAP2>  
F;103,290/Active site: Asp #status predicted

Query Match 35.9%; Score 804; DB 2; Length 509;  
Best Local Similarity 36.4%; Pred. No. 3.6e-59;  
Matches 185; Conservative 51; Mismatches 146; Indels 126; Gaps 8;

QY 6 LLOPILLPLLVNPPSGAT--LIRIPLHR--VOPGRTINLLRGWRPAPLKLKLGAPS- 60  
DB 15 LLOALL-----PASAEGLVRLAKKRIDENSRVAARLSGEGARRLGLAGANSL 65  
QY 61 --PGDKPIFVPLNVRDVOYFGEIGLTPPQNTFAFTGSSNLWVPSRRCHFFSVPCWL 118  
DB 66 GGGGGEGDVALKNTYMAQYFGEIGVGTTPQKFTVFTDGTSSNLWVPSAKC-YFSIACFF 124  
QY 119 HRFDPKASSFCAGTKFAIOYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVF 178  
DB 125 HRYKSGQSSSTYQKNGKPAAIQIGTSGIAGFFSEDSVTGDDLVVKDQEFIEATKEPGLTF 184  
QY 179 AFAHFDGILGLGFPILSVEGPPMDVLVEQGLLDPKPFVSYLNRPDPPEPDGGLVGLGS 238  
DB 185 MVAKFDGILGLGFEISVGDVAVPVVYKVEQGLVSEPVFSFWNRHSDSGEGEIVFGQM 244  
QY 239 DPAHYIPPLTFVVPVPAWQIHMERYKVGPGLT-LCAKGCAAILDTGTSLTGTTEER 297  
DB 245 DPHYKGNHTYVPSQKGYQFEMGDVLIQKTKTGFCASGCAIADSGTSLLAGPTAIT 304  
QY 298 ALHAAITG----- 305  
DB 305 EINEKIGATGVWSQBEKTVVSQYGOQILDLILAETOPSKICQVGLCTFDGKHGVSAGIK 364  
QY 306 -----IPLLAGY 313  
DB 365 SVVDDERAGSNGLSQGMNACEMAVVMQNQLAQNKTQDLILNINQLCDKLPSPMGES 424  
QY 314 IILCSIPKLPVAVFLGGVWNLTAHDYVIOYTRNGVRLCLSGFOALDVPVPPAGPFWIL 373  
DB 425 SVDCGSLASMPFISFTIGAKKFKALDPEYILKVGEGAAAQCISSGTAMDIPPRGFLWIL 484  
QY 374 GDVFLGTYYAVFDGDMKSSARVGLARA 401  
DB 485 GDVFMGAYHTVFDYGM-----RVGFAS 508

RESULT 15  
JC5077  
aspartic proteinase (EC 3.4.23.-) - dog hookworm (Ancylostoma caninum) (fragment)  
N;Alternate names: Acasp; cathepsin D homolog  
C;Species: Ancylostoma caninum  
C;Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 22-Jun-1999  
C;Accession: JC5077  
R;Harrop, S.A.; Prociw, P.; Brindley, P.J.  
Biochem. Biophys. Res. Commun. 227, 294-302, 1996  
A;Title: Acasp, a gene encoding a cathepsin D-like aspartic protease from the hookworm A  
A;Reference number: JC5077; MUID:97011129; PMID:8858139  
A;Accession: JC5077  
A;Molecule type: mRNA  
A;Residues: 1-442 <HAR>  
A;Cross-references: GB:U34888; NID:G1507724; PIDN:AAB06575.1; PID:G1507725  
C;Comment: This enzyme is allergenic in human and contributes to the segmental inflamma  
C;Genetics:  
A;Gene: Acasp  
C;Superfamily: pepsin  
C;Keywords: aspartic proteinase; hydrolase  
F;106,296/Active site: Asp #status predicted

Query Match 35.9%; Score 803.5; DB 2; Length 442;  
Best Local Similarity 47.5%; Pred. No. 3.3e-59;

Matches 160; Conservative 44; Mismatches 126; Indels 7; Gaps 2;  
QY 70 LSNVRDVOYFGEIGLTPPQNTFAFTGSSNLWVPSRRCHFFSVPCWLHHRFPDKASSS 129  
DB 80 LRNTMDAQYFTGIQIGTPAQNTVFTDGTSSNLWVPSRRCHFFHDIACMLHRYDSGASST 139  
QY 130 FOANGTKFAIOYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFPAFAHFDGILGL 189  
DB 140 YKEDGRKMAIOYGTGSMKGFISKDNVCIAGICAEQPPAEATSPGLTFFIAAKFDGILGI 199  
QY 190 GFFILSVEGVPMDVLVEQGLLDPKPFVSYLNRPDPPEPDGGLVGLGSDDPAHVIPPLTF 249  
DB 200 TFPEISVLGVPPVFHTFIEQKVPSPFALNLRNPDSSELGGEITLGGMDTRRIVEPLTW 259  
QY 250 VPVTVPAWQIHMERYKVGPGLT-LCA--KGCACAILDTGTSLTGTTEERIALHAAIGGI 306  
DB 260 TPVTRRGYQFEMDKVQGGSTSIACPNFSCQAIADTGTSLIAGPKAQSASRNSLVLE 319  
QY 307 PLLAGEYIILCSEIPKLPVAVFLGGVWNLTAHDYVIOYTRNGVRLCLSGFOALDVPVPP 366  
DB 320 PTYEGEYMPCDKVPFPPLSFVIEARTFTLKGEDYVLTAKAGGKSIKLSGFMGMDFPER 379  
QY 367 AGPFWILGDVFLGTYYAVFDGDMKSSARVGLARAT 403  
DB 380 IGLMILGDVFIGKYYTVFDVG-----QARLGFAQAKS 412

Search completed: June 2, 2004, 20:22:21  
Job time : 29.59 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:19:10 ; Search time 74.8784 Seconds  
(without alignments)  
1578.054 Million cell updates/sec

Title: US-09-700-770-8

Perfect score: 2238

Sequence: 1 MSPPPLLQLPLLLPLLNVE.....ARTRGADLGMGTAAQFPG 420

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/PCT\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US09D\_PUBCOMB.pep.\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US10F\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2238	100.0	420	12	US-09-968-415-4
2	2238	100.0	420	14	US-10-180-719-4
3	2232	99.7	420	14	US-10-288-222A-30
4	2232	99.7	433	9	US-09-964-899-11
5	2069.5	92.5	395	13	US-10-094-080-3
6	1702.5	76.1	390	9	US-09-969-384-15
7	1560.5	69.7	419	9	US-09-789-919-44
8	1328	59.3	262	9	US-09-915-582-66
9	1328	59.3	262	11	US-09-833-245-1469
10	1328	59.3	262	14	US-10-277-802-66
11	1179	52.7	285	9	US-09-925-302-670
12	1179	52.7	285	12	US-09-925-302-670
13	1050	46.9	212	9	US-09-915-582-87
14	1050	46.9	212	11	US-09-833-245-1471
15	1050	46.9	212	14	US-10-277-802-87

16	1037	46.3	410	11	US-09-833-245-710
17	1015	45.4	412	9	US-09-215-450-25
18	1015	45.4	412	9	US-09-953-956-12
19	1015	45.4	412	12	US-10-275-107-39
20	1015	45.4	412	13	US-10-114-464-12
21	1015	45.4	412	16	US-10-601-091-25
22	1015	45.4	412	16	US-10-408-765A-406
23	1002	44.8	440	12	US-10-112-944-433
24	905.5	40.5	444	15	US-10-369-493-6962
25	887	39.6	446	14	US-10-220-083-2
26	869	38.8	396	9	US-09-215-450-22
27	869	38.8	396	9	US-09-953-956-13
28	869	38.8	396	12	US-10-621-263-9
29	869	38.8	396	13	US-10-114-464-13
30	869	38.8	396	15	US-10-295-027-179
31	869	38.8	396	16	US-10-188-832-54
32	869	38.8	396	16	US-10-601-091-22
33	868	38.8	368	11	US-09-833-245-707
34	868	38.8	404	14	US-10-106-698-6317
35	828.5	37.0	514	14	US-10-339-351-1
36	825.5	36.9	514	14	US-10-339-351-3
37	815	36.4	507	12	US-10-424-599-245585
38	798.5	35.7	523	12	US-10-425-114-57691
39	793	35.4	376	15	US-10-051-874-164
40	790	35.3	374	15	US-10-074-978A-134
41	788	35.2	513	12	US-10-425-114-46548
42	788	35.2	513	12	US-10-425-114-66071
43	787	35.2	480	12	US-10-425-114-65101
44	787	35.2	513	12	US-10-425-114-56631
45	786	35.1	513	12	US-10-425-114-57054

## ALIGNMENTS

### RESULT 1

US-09-968-415-4  
; Sequence 4, Application US/09968415  
; Publication No. US20020086334A1  
; GENEAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Hillman, Jennifer L.  
; Yue, Henry  
; Guegler, Karl J.  
; Corley, Neil C.  
; Tang, Tom Y.  
; Shah, Purvi  
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/968,415  
; FILING DATE: 26-Sep-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/659,151  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mohan-Peterson, Sheela  
; REGISTRATION NUMBER: 41,201  
; REFERENCE/DOCKET NUMBER: PF-0458 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555

```

; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGAST01
; CLONE: 877617
; SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
US-09-968-415-4

Query Match          100.0%; Score 2238; DB 12; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.9e-209;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPPPLQLPLLLLPLLNVEPSGATLIRIPLHRVQPGRTNLLRGWREPAELPKLGAPS 60
DB 1 MSPPPLQLPLLLLPLLNVEPSGATLIRIPLHRVQPGRTNLLRGWREPAELPKLGAPS 60

QY 61 PGDKPIFVPLSNRYRDVQYFGEIGLGTTPQNFTVAEDTGSSNLWVPSRRCHFFSVPCWLHH 120
DB 61 PGDKPIFVPLSNRYRDVQYFGEIGLGTTPQNFTVAEDTGSSNLWVPSRRCHFFSVPCWLHH 120

QY 121 RFDPKASSFQANGTKFAIQYGTGRVDGLSDKLTIGGKASVIFGEALWEPSSLVFAF 180
DB 121 RFDPKASSFQANGTKFAIQYGTGRVDGLSDKLTIGGKASVIFGEALWEPSSLVFAF 180

QY 181 AHFDGILGLGFPILSVGVRPMDVLVEQGLDKPVFSFYLNDRDPEPDGGLVLGGSDP 240
DB 181 AHFDGILGLGFPILSVGVRPMDVLVEQGLDKPVFSFYLNDRDPEPDGGLVLGGSDP 240

QY 241 AHYIPLTFVPTVPAYQIHMERVKVGGLTLCAGCAAIIIDTGTSLITGTETIRALH 300
DB 241 AHYIPLTFVPTVPAYQIHMERVKVGGLTLCAGCAAIIIDTGTSLITGTETIRALH 300

QY 301 AAGGIPPLAGEYIILCSIEIPKLPVSLGGVWFLNLAHDYVIQTRNGVRLCLSGFOA 360
DB 301 AAGGIPPLAGEYIILCSIEIPKLPVSLGGVWFLNLAHDYVIQTRNGVRLCLSGFOA 360

QY 361 LDVPPPPAGFWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLWGGETAQOQFPG 420
DB 361 LDVPPPPAGFWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLWGGETAQOQFPG 420

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RESULT 2

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US-10-180-719-4
; Sequence 4, Application US/10180719
; Publication No. US20030166246A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guégler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi.
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/10/180,719
; FILING DATE: 25-Jun-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271
; FILING DATE: 16-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGAST01
; CLONE: 877617
; SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
US-10-180-719-4

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Query Match          100.0%; Score 2238; DB 14; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.9e-209;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPPPLQLPLLLLPLLNVEPSGATLIRIPLHRVQPGRTNLLRGWREPAELPKLGAPS 60
DB 1 MSPPPLQLPLLLLPLLNVEPSGATLIRIPLHRVQPGRTNLLRGWREPAELPKLGAPS 60

QY 61 PGDKPIFVPLSNRYRDVQYFGEIGLGTTPQNFTVAEDTGSSNLWVPSRRCHFFSVPCWLHH 120
DB 61 PGDKPIFVPLSNRYRDVQYFGEIGLGTTPQNFTVAEDTGSSNLWVPSRRCHFFSVPCWLHH 120

QY 121 RFDPKASSFQANGTKFAIQYGTGRVDGLSDKLTIGGKASVIFGEALWEPSSLVFAF 180
DB 121 RFDPKASSFQANGTKFAIQYGTGRVDGLSDKLTIGGKASVIFGEALWEPSSLVFAF 180

QY 181 AHFDGILGLGFPILSVGVRPMDVLVEQGLDKPVFSFYLNDRDPEPDGGLVLGGSDP 240
DB 181 AHFDGILGLGFPILSVGVRPMDVLVEQGLDKPVFSFYLNDRDPEPDGGLVLGGSDP 240

QY 241 AHYIPLTFVPTVPAYQIHMERVKVGGLTLCAGCAAIIIDTGTSLITGTETIRALH 300
DB 241 AHYIPLTFVPTVPAYQIHMERVKVGGLTLCAGCAAIIIDTGTSLITGTETIRALH 300

QY 301 AAGGIPPLAGEYIILCSIEIPKLPVSLGGVWFLNLAHDYVIQTRNGVRLCLSGFOA 360
DB 301 AAGGIPPLAGEYIILCSIEIPKLPVSLGGVWFLNLAHDYVIQTRNGVRLCLSGFOA 360

QY 361 LDVPPPPAGFWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLWGGETAQOQFPG 420
DB 361 LDVPPPPAGFWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLWGGETAQOQFPG 420

```

RESULT 3

```

US-10-288-222A-30
; Sequence 30, Application US/10288222A
; Publication No. US20030119742A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Galvin, Katherine
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: Methods and Compositions to treat
; TITLE OF INVENTION: Cardiovascular Disease Using 135, 258, 1261, 1486, 2398, 241
; FILE REFERENCE: MPI2001-286P1R(M)
; CURRENT APPLICATION NUMBER: US/10/288,222A
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 30
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-288-222A-30

Query Match      99.7%; Score 2232; DB 14; Length 420;
Best Local Similarity 99.8%; Pred. No. 7.3e-209;
Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPPPLLOPLLLLLPLNVEPSGATLIRIPHRVQPGRTNLRGWRPAPLKLKGLAPS 60
Db 1 MSPPPLLOPLLLLLPLNVEPSGATLIRIPHRVQPGRTNLRGWRPAPLKLKGLAPS 60
QY 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNTFAFDGSSNLWVPSRCHFFSVPCMLHH 120
Db 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNTFAFDGSSNLWVPSRCHFFSVPCMLHH 120
QY 121 RFDPKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180
Db 121 RFDPKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180
QY 181 AHFDGILGLGFPILLSVEGRPPMDVLVBOGLLDKPFVSFYLNRPDPPEPDGGLVILGSDP 240
Db 181 AHFDGILGLGFPILLSVEGRPPMDVLVBOGLLDKPFVSFYLNRPDPPEPDGGLVILGSDP 240
QY 241 AHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALH 300
Db 241 AHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALH 300
QY 301 AATGGIPLLAGETIILCSEIPKLPAYSVFLGGVWFNLTADHYVIQTRNGVRLCLSGFOA 360
Db 301 AATGGIPLLAGETIILCSEIPKLPAYSVFLGGVWFNLTADHYVIQTRNGVRLCLSGFOA 360
QY 361 LDVPPAGPWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLGMGETAQAOFPG 420
Db 361 LDVPPAGPWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLGMGETAQAOFPG 420

RESULT 4
US-964-899-11
; Sequence 11, Application US/09964899
; Patent No. US2002017446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-964-899-11

Query Match      99.7%; Score 2232; DB 9; Length 433;
Best Local Similarity 99.8%; Pred. No. 7.6e-209;
Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPPPLLOPLLLLLPLNVEPSGATLIRIPHRVQPGRTNLRGWRPAPLKLKGLAPS 60
Db 14 MSPPPLLOPLLLLLPLNVEPSGATLIRIPHRVQPGRTNLRGWRPAPLKLKGLAPS 73
QY 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNTFAFDGSSNLWVPSRCHFFSVPCMLHH 120
Db 74 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNTFAFDGSSNLWVPSRCHFFSVPCMLHH 133

; SEQ ID NO 30
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-288-222A-30

Query Match      99.7%; Score 2232; DB 14; Length 420;
Best Local Similarity 99.8%; Pred. No. 7.3e-209;
Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 121 RFDPKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180
Db 134 RFDPKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 193
QY 181 AHFDGILGLGFPILLSVEGRPPMDVLVBOGLLDKPFVSFYLNRPDPPEPDGGLVILGSDP 240
Db 194 AHFDGILGLGFPILLSVEGRPPMDVLVBOGLLDKPFVSFYLNRPDPPEPDGGLVILGSDP 253
QY 241 AHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALH 300
Db 254 AHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALH 313
QY 301 AATGGIPLLAGETIILCSEIPKLPAYSVFLGGVWFNLTADHYVIQTRNGVRLCLSGFOA 360
Db 314 AATGGIPLLAGETIILCSEIPKLPAYSVFLGGVWFNLTADHYVIQTRNGVRLCLSGFOA 373
QY 361 LDVPPAGPWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLGMGETAQAOFPG 420
Db 374 LDVPPAGPWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLGMGETAQAOFPG 433

RESULT 5
US-10-094-080-3
; Sequence 3, Application US/10094080
; Publication No. US20020187140A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/094,080
; FILING DATE: 07-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/387,413
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0125 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; LIBRARY: LUNGN020
; CLONE: 312099
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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US-10-094-080-3

Query Match 92.5%; Score 2069.5; DB 13; Length 395;  
Best Local Similarity 93.8%; Pred. No. 4.8e-193;  
Matches 394; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

QY 1 MSPPPLOPLLLPLLVNPSGATLIRPLHRVQGRRTLLNRGWREPAELPKLGAPS 60  
DB 1 MSPPPLOPLLLPLLVNPSGATLIRPLHRVQGRRTLLNRGWREPAELPKLGAPS 60

QY 61 PGDKPIFVPLSNRYRDVQFGEIGLTPPQNFVAEDTSSNLWPSRRCHFFSVPCWLHH 120  
DB 61 PGDKPIFVPLSNRYRDVQFGEIGLTPPQNFVAEDTSSNLWPSRRCHFFSVPCWLHH 120

QY 121 RPDPKASSFQANGKFAIQVGTGRVDGILSDKLTIGIKGASVIFGEALWEPSELVAF 180  
DB 121 RPDPKASSFQANGKFAIQVGTGRVDGILSDKLTIGIKGASVIFGEALWEPSELVAF 180

QY 181 AHFDGILGFPILSVGVRPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVILGSDP 240  
DB 181 AHFDGILGFPILSVGVRPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVILGSDP 240

QY 241 AHYIPLTFVPTVAYQIHMERVKGPGGLTLCAKGCALIDTGTSLITGTEIRALH 300  
DB 241 AHYIPLTFVPTVAYQIHMERVKGPGGLTLCAKGCALIDTGTSLITGTEIRALH 300

QY 301 AAGIGPILAGBYIILCSEIPKLPVAVFDRGDMKSSARVGLARTRGADLWGETAQAQFP 360  
DB 301 AAGIGPILAGBYIILCSEIPKLPVAVFDRGDMKSSARVGLARTRGADLWGETAQAQFP 360

QY 361 LDVPPPAGEFWILGDFVLTGYVAVFDRGDMKSSARVGLARTRGADLWGETAQAQFP 420  
DB 361 LDVPPPAGEFWILGDFVLTGYVAVFDRGDMKSSARVGLARTRGADLWGETAQAQFP 420

## RESULT 6

US-09-969-384-15  
; Sequence 15, Application US/09969384  
; Publication No. US20020192749A1  
; GENERAL INFORMATION:  
; APPLICANT: Moore, et al.  
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies  
; FILE REFERENCE: PT055PI  
; CURRENT APPLICATION NUMBER: US/09/969,384  
; PRIOR FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: PCT/US01/10542  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: 60/236,384  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/194,118  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-969-384-15

Query Match 76.1%; Score 1702.5; DB 9; Length 390;  
Best Local Similarity 83.3%; Pred. No. 3.1e-157;  
Matches 334; Conservative 7; Mismatches 15; Indels 45; Gaps 4;

QY 21 PSGATLIRPLHRVQGRRTLLNRGWREPAELPKLGAPSPGDKPIFVPLSNRYRDVQYFG 80  
DB 34 PSGATLIRPLHRVQGRRTLLNRGWREPAELPKLGAPSPGDKPIFVPLSNRYRDVQYFG 80

QY 81 EIGLGTTPQNFVAEDTSSNLWPSRRCHFFSVPCWLHHRFDPKASSFQANGTKFAIQ 140  
DB 89 -----WLHHRFDPKASTP-SSQWDQFAIQ 111

QY 141 YGTRVDGILSDKLTIGIKGASVIFGE-ALWEPSELVAFPAHFDDGILGFPILSVG 199

DB 112 YGTRVHGILSDKLTIGIKGASVIFGEALSGTQFGL--RFPDPDGLGFGPILSVG 169

QY 200 RPPMDVLVEQGLLDKPVFSFYLNRDPEPDGGELVILGSDPAHYIPLTFVPTVTPAYWQ 259

DB 170 RPPMDVLVEQGLLDKPVFSFYLNRDPEPDGGELVILGSDPAHYIPLTFVPTVTPAYWQ 229

QY 260 IHMERVKVGPGLTLCAGCAAILDTGTSLITGPTTEIRALHAAIGGIPLLAGYIILCSE 319

DB 230 IHMERVKVGPGLTLCAGCAAILDTGTSLITGPTTEIRALHAAIGGIPLLAGYIILCSE 289

QY 320 IPKLPVAVFDRGDMKSSARVGLARTRGADLWGETAQAQFP 420

DB 290 IPKLPVAVFDRGDMKSSARVGLARTRGADLWGETAQAQFP 390

QY 380 TYVAVFDRGDMKSSARVGLARTRGADLWGETAQAQFP 420

DB 350 TYVAVFDRGDMKSSARVGLARTRGADLWGETAQAQFP 390

## RESULT 7

US-09-783-919-44  
; Sequence 44, Application US/09789919  
; Patent No. US2002006485A1  
; GENERAL INFORMATION:  
; APPLICANT: Lemischka, Ihor  
; APPLICANT: Moore, Kateri  
; TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM  
; FILE REFERENCE: 2275-1-005  
; CURRENT APPLICATION NUMBER: US/09/789,919  
; CURRENT FILING DATE: 2001-02-21  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 419  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-783-919-44

Query Match 69.7%; Score 1560.5; DB 9; Length 419;  
Best Local Similarity 70.3%; Pred. No. 2.5e-143;  
Matches 296; Conservative 37; Mismatches 79; Indels 9; Gaps 3;

QY 7 LQPLLLPLLL--NVPSGATLIRPLHRVQGRRTLLNRGWREPAELPKLGAPSPGD 63  
DB 1 MSPLLLLCLLLGNLEPEEAKLIRVPLQRIHLGHRILNPLNGWEQLAELSR--TSTSGG 58

QY 64 KPIFVPLSNRYRDVQFGEIGLTPPQNFVAEDTSSNLWPSRRCHFFSVPCWLHHRFD 123  
DB 59 NPSFVPLSKFMNTQYFGTIGLTPPQNFVAEDTSSNLWPSRRCHFFSVPCWLHHRFD 118

QY 124 PKASSFQANGTKFAIQVGTGRVDGILSDKLTIGIKGASVIFGEALWEPSELVAF 183  
DB 119 PKASSFQANGTKFAIQVGTGRVDGILSDKLTIGIKGASVIFGEALWEPSELVAF 178

QY 184 DGILGFPILSVGVRPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVILGSDPAHY 243  
DB 179 DGILGFPILSVGVRPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVILGSDPAHY 238

QY 244 IPPLTFVPTVAYQIHMERVKGPGGLTLCAKGCALIDTGTSLITGTEIRALHAAI 303  
DB 239 VPPLTFVPTVAYQIHMERVKGPGGLTLCAKGCALIDTGTSLITGTEIRALHAAI 298

QY 304 GGIPILAGBYIILCSEIPKLPVAVFDRGDMKSSARVGLARTRGADLWGETAQAQFP 363  
DB 299 GGIPILAGBYIILCSEIPKLPVAVFDRGDMKSSARVGLARTRGADLWGETAQAQFP 358

QY 364 PPDGPFVILGDFVLTGYVAVFDRGDMKSSARVGLARTRGADLWGETAQAQFP 419  
DB 359 PPDGPFVILGDFVLTGYVAVFDRGDMKSSARVGLARTRGADLWGETAQAQFP 418

QY 420 G 420

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Db 419 G 419
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1469
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (231)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-1469

Query Match 59.3%; Score 1328; DB 11; Length 262;
Best Local Similarity 97.6%; Pred. No. 6.2e-121;
Matches 249; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MSPPPQLQPLLLPLLNVEPSGATLIRIPLRVQPGRRITLIRGWRPAELPKLGAPS 60
Db 1 MSPPPQLQPLLLPLLNVEPSGATLIRIPLRVQPGRRITLIRGWRPAELPKLGAPS 60
Qy 61 PGDKPIFVPLSNRYDVQYFGIIGLTPQNTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPIFVPLSNRYDVQYFGIIGLTPQNTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
Qy 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKASVIFGEALWEPVSLVFAF 180
Db 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKASVIFGEALWEPVSLVFAF 180
Qy 181 AHFDGILGLGFPILSVGVRRPMDVLVEQGLDKPVFSFYLNRPDPEEPDGGELVLGGSDP 240
Db 181 AHFDGILGLGFPILSVGVRRPMDVLVEQGLDKPVFSFYLNRPDPEEPDGGELVLGGSDP 240
Qy 241 AHYIPPLTFVPTVP 255
Db 241 AHYIPPSFVVRSP 255

RESULT 10
US-10-277-802-66
; Sequence 66, Application US/10277802
; Publication No. US2003019070A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723p1
; CURRENT APPLICATION NUMBER: US/10/277,802
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 09/915,582
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (231)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-277-802-66

Query Match 59.3%; Score 1328; DB 14; Length 262;
Best Local Similarity 97.6%; Pred. No. 6.2e-121;
Matches 249; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 419 G 419
; Sequence 66, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723p1
; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (231)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-915-582-66

Query Match 59.3%; Score 1328; DB 9; Length 262;
Best Local Similarity 97.6%; Pred. No. 6.2e-121;
Matches 249; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MSPPPQLQPLLLPLLNVEPSGATLIRIPLRVQPGRRITLIRGWRPAELPKLGAPS 60
Db 1 MSPPPQLQPLLLPLLNVEPSGATLIRIPLRVQPGRRITLIRGWRPAELPKLGAPS 60
Qy 61 PGDKPIFVPLSNRYDVQYFGIIGLTPQNTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPIFVPLSNRYDVQYFGIIGLTPQNTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
Qy 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKASVIFGEALWEPVSLVFAF 180
Db 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKASVIFGEALWEPVSLVFAF 180
Qy 181 AHFDGILGLGFPILSVGVRRPMDVLVEQGLDKPVFSFYLNRPDPEEPDGGELVLGGSDP 240
Db 181 AHFDGILGLGFPILSVGVRRPMDVLVEQGLDKPVFSFYLNRPDPEEPDGGELVLGGSDP 240
Qy 241 AHYIPPLTFVPTVP 255
Db 241 AHYIPPSFVVRSP 255

RESULT 9
US-09-833-245-1469
; Sequence 1469, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
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QY 1 MSPBLLQPLLLPLLVPSGATLIRIPLHRVQGRRTLNLLRGWREPAELPKLGAPS 60
Db 1 MSPBLLQPLLLPLLVPSGATLIRIPLHRVQGRRTLNLLRGWREPAELPKLGAPS 60
QY 61 PGDKPIFVPLSNRYRDVQVFGIIGLGTTPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPIFVPLSNRYRDVQVFGIIGLGTTPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
QY 121 RPDPKASSFQANGTKFAIQYGTGRVDGILSDKLTIGGIKASVIFGEALWEPSSLVFAF 180
Db 121 RPDPKASSFQANGTKFAIQYGTGRVDGILSDKLTIGGIKASVIFGEALWEPSSLVFAF 180
QY 181 AHFDGILGLGFPILSVGVRRPMDVLVEQGLLDKVPFSFYLNRPDPEPDGGELVLGGSDP 240
Db 181 AHFDGILGLGFPILSVGVRRPMDVLVEQGLLDKVPFSFYLNRPDPEPDGGELVLGGSDP 240
QY 241 AHYIPPLTFVPTVP 255
Db 241 AHYIPSPFVVRSP 255
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## RESULT 11

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US-09-925-302-670
Query Match 52.7%; Score 1179; DB 9; Length 285;
Best Local Similarity 80.7%; Pred. No. 2.4e-106;
Matches 230; Conservative 4; Mismatches 9; Indels 42; Gaps 2;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 670
LENGTH: 285
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-302-670
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QY 21 PSGATLIRIPLHRVQGRRTLNLLRGWREPAELPKLGAPSPGDKPIFVPLSNRYRDVQVFG 80
Db 43 PSGATLIRIPLHRVQGRRTLNLLRGWREPAELPKLGAPSPEDKPIFVPLSNYKG----- 97
QY 81 EIGLGTTPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSFQANGTKFAIQ 140
Db 98 -----WLHHRFDPKASTP-SSQWDQFAIQ 120
QY 141 YGTGRVDGILSDKLTIGGIKASVIFGEALWEPSSLVFAFAHFDGILGFPILSVGVRR 200
Db 121 YGTGRVHGILSDKLTIGGIKASVIFGEALWEPSSLVFAFAHFDGILGFPILSVGVRR 180
QY 201 PMDVLVEQGLLDKVPFSFYLNRPDPEPDGGELVLGGSDPAHYIPPLTFVPTVPYAWQI 260
Db 181 PMDVLVEQGLLDKVPFSFYLNRPDPEPDGGELVLGGSDPAHYIPPLTFVPTVPYAWQI 240
QY 261 HMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALHAAIGG 305
Db 241 HMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALHAAIGG 285
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## RESULT 12

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US-09-925-302-670
Query Match 52.7%; Score 1179; DB 9; Length 285;
Best Local Similarity 80.7%; Pred. No. 2.4e-106;
Matches 230; Conservative 4; Mismatches 9; Indels 42; Gaps 2;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 670
LENGTH: 285
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-302-670
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```
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 670
LENGTH: 285
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-302-670
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Query Match 52.7%; Score 1179; DB 12; Length 285;
Best Local Similarity 80.7%; Pred. No. 2.4e-106;
Matches 230; Conservative 4; Mismatches 9; Indels 42; Gaps 2;
QY 21 PSGATLIRIPLHRVQGRRTLNLLRGWREPAELPKLGAPSPGDKPIFVPLSNRYRDVQVFG 80
Db 43 PSGATLIRIPLHRVQGRRTLNLLRGWREPAELPKLGAPSPEDKPIFVPLSNYKG----- 97
QY 81 EIGLGTTPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSFQANGTKFAIQ 140
Db 98 -----WLHHRFDPKASTP-SSQWDQFAIQ 120
QY 141 YGTGRVDGILSDKLTIGGIKASVIFGEALWEPSSLVFAFAHFDGILGFPILSVGVRR 200
Db 121 YGTGRVHGILSDKLTIGGIKASVIFGEALWEPSSLVFAFAHFDGILGFPILSVGVRR 180
QY 201 PMDVLVEQGLLDKVPFSFYLNRPDPEPDGGELVLGGSDPAHYIPPLTFVPTVPYAWQI 260
Db 181 PMDVLVEQGLLDKVPFSFYLNRPDPEPDGGELVLGGSDPAHYIPPLTFVPTVPYAWQI 240
QY 261 HMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALHAAIGG 305
Db 241 HMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALHAAIGG 285
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## RESULT 13

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US-09-915-582-87
Query Match 52.7%; Score 1179; DB 9; Length 285;
Best Local Similarity 80.7%; Pred. No. 2.4e-106;
Matches 230; Conservative 4; Mismatches 9; Indels 42; Gaps 2;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 17 Human Secreted Proteins
FILE REFERENCE: PS723P1
CURRENT APPLICATION NUMBER: US/09/915,582
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: PCT/US01/01431
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/231,968
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 87
LENGTH: 212
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (9)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-915-582-87
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Query Match 46.9%; Score 1050; DB 9; Length 212;  
Best Local Similarity 100.0%; Pred. No. 6.2e-94;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DPEPDGGLVGGSDPAHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILD 283  
DB 16 DPEPDGGLVGGSDPAHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILD 75

QY 284 TGTSLITGPTTEIRALHAAIGGIPLLAGEYIILCSEIPKLPAYSVFLGGVWFNLTADYV 343  
DB 76 TGTSLITGPTTEIRALHAAIGGIPLLAGEYIILCSEIPKLPAYSVFLGGVWFNLTADYV 135

QY 344 IQTTRNGVRLCLSGFQALDVPDPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARAT 403  
DB 136 IQTTRNGVRLCLSGFQALDVPDPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARAT 195

QY 404 RGADLWGGETAQAFP 420  
DB 196 RGADLWGGETAQAFP 212

## RESULT 14

US-09-833-245-1471  
; Sequence 1471, Application US/09833245  
; Publication No. US20040010134A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF546PCT  
; CURRENT APPLICATION NUMBER: US/09/833,245  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229,358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256,931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199,384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 2267  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1471  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (9)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-833-245-1471

Query Match 46.9%; Score 1050; DB 11; Length 212;  
Best Local Similarity 100.0%; Pred. No. 6.2e-94;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DPEPDGGLVGGSDPAHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILD 283  
DB 16 DPEPDGGLVGGSDPAHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILD 75

QY 284 TGTSLITGPTTEIRALHAAIGGIPLLAGEYIILCSEIPKLPAYSVFLGGVWFNLTADYV 343  
DB 76 TGTSLITGPTTEIRALHAAIGGIPLLAGEYIILCSEIPKLPAYSVFLGGVWFNLTADYV 135

QY 344 IQTTRNGVRLCLSGFQALDVPDPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARAT 403  
DB 136 IQTTRNGVRLCLSGFQALDVPDPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARAT 195

QY 404 RGADLWGGETAQAFP 420  
DB 196 RGADLWGGETAQAFP 212

## RESULT 15

US-10-277-802-87  
; Sequence 87, Application US/10277802

Publication No. US20030190707A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 17 Human Secreted Proteins  
; FILE REFERENCE: PS723P1  
; CURRENT APPLICATION NUMBER: US/10/277,802  
; CURRENT FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: 09/915,582  
; PRIOR FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: PCT/US01/01431  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/231,968  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (9)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-277-802-87

Query Match 46.9%; Score 1050; DB 14; Length 212;  
Best Local Similarity 100.0%; Pred. No. 6.2e-94;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DPEPDGGLVGGSDPAHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILD 283  
DB 16 DPEPDGGLVGGSDPAHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILD 75

QY 284 TGTSLITGPTTEIRALHAAIGGIPLLAGEYIILCSEIPKLPAYSVFLGGVWFNLTADYV 343  
DB 76 TGTSLITGPTTEIRALHAAIGGIPLLAGEYIILCSEIPKLPAYSVFLGGVWFNLTADYV 135

QY 344 IQTTRNGVRLCLSGFQALDVPDPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARAT 403  
DB 136 IQTTRNGVRLCLSGFQALDVPDPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARAT 195

QY 404 RGADLWGGETAQAFP 420  
DB 196 RGADLWGGETAQAFP 212

Search completed: June 2, 2004, 20:25:19  
Job time : 75.8784 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:16:40 ; Search time 29.2707 Seconds  
(without alignments)  
740.773 Million cell updates/sec

Title: US-09-700-770-8  
Perfect score: 2238  
Sequence: 1 MSPPPLQLPLLLLLLNVE.....ARTRGADLGNGETAQAQFFG 420

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PGTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2238	100.0	420	3	US-09-008-271A-4
2	2238	100.0	420	4	US-09-705-448-1
3	2232	99.7	420	3	US-08-974-691-8
4	2069.5	92.5	395	1	US-08-723-338-3
5	2069.5	92.5	395	2	US-09-080-538-3
6	2069.5	92.5	395	4	US-09-387-413-3
7	1897	84.8	445	3	US-08-974-691-6
8	1897	84.8	451	3	US-08-974-691-2
9	1877	83.9	433	4	US-09-705-448-3
10	1564.5	69.9	419	3	US-08-974-691-3
11	1560.5	69.7	419	4	US-09-705-448-10
12	1015	45.4	412	1	US-08-208-007A-12
13	1015	45.4	412	3	US-08-974-691-4
14	1015	45.4	412	4	US-08-915-085A-12
15	1015	45.4	412	4	US-08-798-096-12
16	1015	45.4	412	4	US-08-798-095A-12
17	1015	45.4	412	4	US-09-953-956-12
18	1015	45.4	412	4	US-08-553-125A-12
19	1015	45.4	412	4	US-09-215-450-25
20	1015	45.4	412	4	US-10-114-464-12
21	869	38.8	396	1	US-08-208-007A-13
22	869	38.8	396	3	US-09-032-523-9
23	869	38.8	396	4	US-08-915-095A-13
24	869	38.8	396	4	US-08-798-096-13
25	869	38.8	396	4	US-08-798-095A-13
26	869	38.8	396	4	US-09-953-956-13
27	869	38.8	396	4	US-08-553-125A-13

28	869	38.8	396	4	US-09-802-633-9	Sequence 9, Appli
29	869	38.8	396	4	US-09-215-450-22	Sequence 22, Appli
30	869	38.8	396	4	US-10-114-464-13	Sequence 13, Appli
31	779	34.8	406	4	US-09-215-450-26	Sequence 26, Appli
32	759.5	33.9	388	4	US-09-215-450-23	Sequence 23, Appli
33	729	32.6	326	4	US-09-604-608-31	Sequence 31, Appli
34	708.5	31.7	349	3	US-09-032-523-3	Sequence 3, Appli
35	708.5	31.7	349	4	US-09-802-633-3	Sequence 3, Appli
36	705.5	31.5	398	1	US-08-328-314-2	Sequence 2, Appli
37	705.5	31.5	398	1	US-08-731-045-2	Sequence 2, Appli
38	693.5	31.0	409	1	US-09-640-305-6	Sequence 6, Appli
39	693.5	31.0	409	1	US-08-360-673-6	Sequence 6, Appli
40	691.5	30.9	397	3	US-09-079-415-2	Sequence 2, Appli
41	668.5	29.9	388	4	US-09-215-450-24	Sequence 24, Appli
42	666	29.8	410	1	US-08-088-633-2	Sequence 2, Appli
43	666	29.8	410	1	US-08-245-756-2	Sequence 2, Appli
44	666	29.8	410	1	US-08-441-750-2	Sequence 2, Appli
45	666	29.8	410	2	US-08-441-751-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-008-271A-4  
; Sequence 4, Application US/09008271A  
; Patent No. 6203979  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Hillman, Jennifer L.  
; Yue, Henry  
; Guegler, Karl J.  
; Corley, Neil C.  
; Tang, Tom Y.  
; Shah, Purvi  
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ For Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,271A  
; FILING DATE: 16-Jan-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mohan-Peterson, Shesha  
; REGISTRATION NUMBER: 41,201  
; REFERENCE/DOCKET NUMBER: PF-0458 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 420 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: LUNGAST01  
; CLONE: 877617  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4 :  
US-09-008-271A-4

Query Match 100.0%; Score 2238; DB 3; Length 420;  
Best Local Similarity 100.0%; Pred. No. 2e-222;  
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPPPQLQLLLPLLVNPSGATLIRIPLHRVQFGRRTNLLRGWREPAELPKLGAPS 60  
DB 1 MSPPPQLQLLLPLLVNPSGATLIRIPLHRVQFGRRTNLLRGWREPAELPKLGAPS 60

QY 61 PGDKPIFVPLSNRYDVQYFGEIGLTPPQNFVAFDTGSSNLWVPSRCHFFSVPCWLHH 120  
DB 61 PGDKPIFVPLSNRYDVQYFGEIGLTPPQNFVAFDTGSSNLWVPSRCHFFSVPCWLHH 120

QY 121 RFDPKASSSQANGTKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEALWEPFLVAF 180  
DB 121 RFDPKASSSQANGTKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEALWEPFLVAF 180

QY 181 AHFDGILGFPILSVGVRPMDVLEQGLDKPVSFYLNRPDPPEPDGSELVLGSDP 240  
DB 181 AHFDGILGFPILSVGVRPMDVLEQGLDKPVSFYLNRPDPPEPDGSELVLGSDP 240

QY 241 AHYIPPLTFVPTVPAYQIHMERYKVGPGLTLCAGCAAIIIDTGTSLITGPTTEIRALH 300  
DB 241 AHYIPPLTFVPTVPAYQIHMERYKVGPGLTLCAGCAAIIIDTGTSLITGPTTEIRALH 300

QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVFDGMDKSSARVGLARARTRGADLGMGTAAQPPG 420  
DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVFDGMDKSSARVGLARARTRGADLGMGTAAQPPG 420

RESULT 2

US-09-705-448-1  
; Sequence 1, Application US/09705448  
; Patent No. 6432690  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Hong  
; APPLICANT: Bruno, Sandra A.  
; APPLICANT: Eisenboos, Laura A.  
; APPLICANT: Fogliano, Michael  
; APPLICANT: Cohan, Victoria L.  
; APPLICANT: Bandman, Olga  
; TITLE OF INVENTION: HUMAN ASPARTIC PROTEASES  
; FILE REFERENCE: PF-0458-1 CIP  
; CURRENT APPLICATION NUMBER: US/09/705,448  
; CURRENT FILING DATE: 2000-11-02  
; PRIOR APPLICATION NUMBER: 09/116,641  
; PRIOR FILING DATE: 1998-07-16  
; PRIOR APPLICATION NUMBER: 09/008,271  
; PRIOR FILING DATE: 1998-01-16  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
; FEATURE:  
; OTHER INFORMATION: 372637, LUNGNOT02  
US-09-705-448-1

Query Match 100.0%; Score 2238; DB 4; Length 420;  
Best Local Similarity 100.0%; Pred. No. 2e-222;  
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPPPQLQLLLPLLVNPSGATLIRIPLHRVQFGRRTNLLRGWREPAELPKLGAPS 60  
DB 1 MSPPPQLQLLLPLLVNPSGATLIRIPLHRVQFGRRTNLLRGWREPAELPKLGAPS 60

QY 61 PGDKPIFVPLSNRYDVQYFGEIGLTPPQNFVAFDTGSSNLWVPSRCHFFSVPCWLHH 120

DB 61 PGDKPIFVPLSNRYDVQYFGEIGLTPPQNFVAFDTGSSNLWVPSRCHFFSVPCWLHH 120

QY 121 RFDPKASSSQANGTKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEALWEPFLVAF 180

DB 121 RFDPKASSSQANGTKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEALWEPFLVAF 180

QY 181 AHFDGILGFPILSVGVRPMDVLEQGLDKPVSFYLNRPDPPEPDGSELVLGSDP 240

DB 181 AHFDGILGFPILSVGVRPMDVLEQGLDKPVSFYLNRPDPPEPDGSELVLGSDP 240

QY 241 AHYIPPLTFVPTVPAYQIHMERYKVGPGLTLCAGCAAIIIDTGTSLITGPTTEIRALH 300

DB 241 AHYIPPLTFVPTVPAYQIHMERYKVGPGLTLCAGCAAIIIDTGTSLITGPTTEIRALH 300

QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVFDGMDKSSARVGLARARTRGADLGMGTAAQPPG 420

DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVFDGMDKSSARVGLARARTRGADLGMGTAAQPPG 420

RESULT 3

US-08-974-691-8  
; Sequence 8, Application US/08974691  
; Patent No. 6225103  
; GENERAL INFORMATION:  
; APPLICANT: Keolach, Gerald  
; APPLICANT: Lin, Xinli  
; APPLICANT: Tang, Jordan  
; TITLE OF INVENTION: Cloning and Characterization of Napsin  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center, 1201 W. Peachtree  
; STREET: St.  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30109-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,691  
; FILING DATE: 20-NOV-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/031,196  
; FILING DATE: 20-NOV-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/046,126  
; FILING DATE: 09-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMRF 166  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-873-8794  
; TELEFAX: 404-873-8795  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 420 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-974-691-8

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Query Match          99.7%; Score 2232; DB 3; Length 420;
Best Local Similarity 99.8%; Pred. No. 8.5e-222;
Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPPPLLQPLLLPLLNVEPSGATLIRIPLHRVQPGRRITNLLRGWREPAELPKLGAPS 60
DB 1 MSPPPLLQPLLLPLLNVEPSGATLIRIPLHRVQPGRRITNLLRGWREPAELPKLGAPS 60
QY 61 PGDKPIFVPLSNRYDVOYGEIGLGTTPQNTFAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
DB 61 PGDKPIFVPLSNRYDVOYGEIGLGTTPQNTFAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
QY 121 RFPDKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180
DB 121 RFPDKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180
QY 181 AHFDGILGLGFPILSVGVRPPMDVLVEQGLLDKPVFSFYLNDRDPPEPDGSELVLGSDP 240
DB 181 AHFDGILGLGFPILSVGVRPPMDVLVEQGLLDKPVFSFYLNDRDPPEPDGSELVLGSDP 240
QY 241 AHYIPPLTFVPTVPAYWQIHMERSVKVPGGLTICAKGCAAILDTGTSITGPTTEIRALH 300
DB 241 AHYIPPLTFVPTVPAYWQIHMERSVKVPGGLTICAKGCAAILDTGTSITGPTTEIRALH 300
QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTADHYVITQTRNGVRLCISGFOA 360
DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTADHYVITQTRNGVRLCISGFOA 360
QY 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLWGGETAQAOFP 420
DB 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLWGGETAQAOFP 420

RESULT 4
US-08-723-938-3
; Sequence 3, Application US/08723938
; Patent No. 5776759
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,938
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0125 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
LIBRARY: LUNGN0T02
CLONE: 312099
US-08-723-938-3

Query Match          92.5%; Score 2069.5; DB 1; Length 395;
Best Local Similarity 93.8%; Pred. No. 4.6e-205;
Matches 394; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

QY 1 MSPPPLLQPLLLPLLNVEPSGATLIRIPLHRVQPGRRITNLLRGWREPAELPKLGAPS 60
DB 1 MSPPPLLQPLLLPLLNVEPSGATLIRIPLHRVQPGRRITNLLRGWREPAELPKLGAPS 60
QY 61 PGDKPIFVPLSNRYDVOYGEIGLGTTPQNTFAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
DB 61 PGDKPIFVPLSNRYDVOYGEIGLGTTPQNTFAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
QY 121 RFPDKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180
DB 121 RFPDKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180
QY 181 AHFDGILGLGFPILSVGVRPPMDVLVEQGLLDKPVFSFYLNDRDPPEPDGSELVLGSDP 240
DB 181 AHFDGILGLGFPILSVGVRPPMDVLVEQGLLDKPVFSFYLNDRDPPEPDGSELVLGSDP 240
QY 241 AHYIPPLTFVPTVPAYWQIHMERSVKVPGGLTICAKGCAAILDTGTSITGPTTEIRALH 300
DB 241 AHYIPPLTFVPTVPAYWQIHMERSVKVPGGLTICAKGCAAILDTGTSITGPTTEIRALH 300
QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTADHYVITQTRNGVRLCISGFOA 360
DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTADHYVITQTRNGVRLCISGFOA 360
QY 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLWGGETAQAOFP 420
DB 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLWGGETAQAOFP 420

RESULT 5
US-09-080-538-3
; Sequence 3, Application US/09080538
; Patent No. 5965129
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,538
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/723,938
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0125 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT02
; CLONE: 312099
; US-09-080-538-3

Query Match          92.5%; Score 2069.5; DB 2; Length 395;
Best Local Similarity 93.8%; Pred. No. 4.6e-205;
Matches 394; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

QY 1 MSPPPQLQPLLLLLPLLNVPESGATLIRPLHRVQPGRTLNLLRGWREPAELPKLGAPS 60
DB 1 MSPPPQLQPLLLLLPLLNVPESGATLIRPLHRVQPGRTLNLLRGWREPAELPKLGAPS 60
QY 61 PGDKPIFVPLSNYRDVQYFGEIGLTGTPQNFVAEDTGSNLMWPSRCHFFSVPCWLHH 120
DB 61 PGDKPIFVPLSNYRDVQYFGEIGLTGTPQNFVAEDTGSNLMWPSRCHFFSVPCWLHH 120
QY 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSDKLTIGGIKASVIFGEALWEPVLVAF 180
DB 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSDKLTIGGIKASVIFGEALWEPVLVAF 180
QY 181 AHFDGILGFPILSVEGVRRPMDVLEQGLLDKVPFSFYLNRPDPPEPDGGLVILGSDP 240
DB 181 AHFDGILGFPILSVEGVRRPMDVLEQGLLDKVPFSFYLNRPDPPEPDGGLVILGSDP 240
QY 241 AHYIPLTFVPTVPAYQIHMERYKVGPGTLCAKGCALDGTSLITGTEIRALH 300
DB 241 AHYIPLTFVPTVPAYQIHMERYKVGPGTLCAKGCALDGTSLITGTEIRALH 300
QY 301 AAGIGIPLLAGYIILCSEIPKLPVSVFLGGVWFLNLTADHYVIQTRNGVRLCLSGFQA 360
DB 301 AAGIGIPLLAGYIILCSEIPKLPVSVFLGGVWFLNLTADHYVIQTRN----- 349
QY 361 LDVPPAGFWILGDVFLGTYYAVFDRGDMKSSARVGLARARTRGADLWGETAQAQPPG 420
DB 350 -----DVFLGTYYAVFDRGDMKSSARVGLARARTRGADLWGETAQAQPPG 395

RESULT 6
US-09-387-413-3
; Sequence 3, Application US/09387413
; Patent No. 6475485
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Coleman, Roger
; TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
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; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,413
; FILING DATE: 31-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/080,538
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0125 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT02
; CLONE: 312099
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-387-413-3
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Query Match          92.5%; Score 2069.5; DB 4; Length 395;
Best Local Similarity 93.8%; Pred. No. 4.6e-205;
Matches 394; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

QY 1 MSPPPQLQPLLLLLPLLNVPESGATLIRPLHRVQPGRTLNLLRGWREPAELPKLGAPS 60
DB 1 MSPPPQLQPLLLLLPLLNVPESGATLIRPLHRVQPGRTLNLLRGWREPAELPKLGAPS 60
QY 61 PGDKPIFVPLSNYRDVQYFGEIGLTGTPQNFVAEDTGSNLMWPSRCHFFSVPCWLHH 120
DB 61 PGDKPIFVPLSNYRDVQYFGEIGLTGTPQNFVAEDTGSNLMWPSRCHFFSVPCWLHH 120
QY 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSDKLTIGGIKASVIFGEALWEPVLVAF 180
DB 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSDKLTIGGIKASVIFGEALWEPVLVAF 180
QY 181 AHFDGILGFPILSVEGVRRPMDVLEQGLLDKVPFSFYLNRPDPPEPDGGLVILGSDP 240
DB 181 AHFDGILGFPILSVEGVRRPMDVLEQGLLDKVPFSFYLNRPDPPEPDGGLVILGSDP 240
QY 241 AHYIPLTFVPTVPAYQIHMERYKVGPGTLCAKGCALDGTSLITGTEIRALH 300
DB 241 AHYIPLTFVPTVPAYQIHMERYKVGPGTLCAKGCALDGTSLITGTEIRALH 300
QY 301 AAGIGIPLLAGYIILCSEIPKLPVSVFLGGVWFLNLTADHYVIQTRNGVRLCLSGFQA 360
DB 301 AAGIGIPLLAGYIILCSEIPKLPVSVFLGGVWFLNLTADHYVIQTRN----- 349
QY 361 LDVPPAGFWILGDVFLGTYYAVFDRGDMKSSARVGLARARTRGADLWGETAQAQPPG 420
DB 350 -----DVFLGTYYAVFDRGDMKSSARVGLARARTRGADLWGETAQAQPPG 395
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RESULT 7  
US-08-974-691-6



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; Sequence 6, Application US/08974691
; Patent No. 6225103
; GENERAL INFORMATION:
; APPLICANT: Keolsch, Gerald
; APPLICANT: Lin, Xinli
; APPLICANT: Tang, Jordan
; TITLE OF INVENTION: Cloning and Characterization of Napsin
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 W. Peachtree
; STREET: St.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,691
; FILING DATE: 20-NOV-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,196
; FILING DATE: 20-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/046,126
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRP 166
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-974-691-6

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Query Match      84.8%; Score 1897; DB 3; Length 445;
Best Local Similarity 86.0%; Pred. No. 3.6e-187;
Matches 361; Conservative 16; Mismatches 43; Indels 0; Gaps 0;

Qy 1 MSPPELLOPLLLPLLNVPESGATLIRPLHRVQPGRTTLNLRGWREPAELPKLGAPS 60
Db 1 MSPPELLOPLLLPLLNVPESGATLIRPLHRVQPGRTTLNLRGWREPAELPKLGAPS 60

Qy 61 PGDKPIFVPLSNRVDVQFGEIGLGTTPQNTFVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPASVPLSKFLDAQYFGEIGLGTTPQNTFVAFDTGSSNLWVPSRRCHFFSVPCWFHH 120

Qy 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAF 180
Db 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAF 180

Qy 181 AHFGGILGLGPPILSVRGVRRPMDVLVEQGLLDPKPVFSFYLNRPDPDPGELVVGSDP 240
Db 181 SRPDGILGLGPPILSVRGVRRPMDVLVEQGLLDPKPVFSFYLNRPDPDPGELVVGSDP 240

Qy 241 AHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAALTDGTSLITGPTTEIRALH 300
Db 241 AHYIPPLTFVPTVPAYWQHMERVKVGSRLTLCAGCAALTDGTSLITGPTTEIRALH 300

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Qy 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSLGGVWFLTAHDYVVIQTRNGVRLCLSGFOA 360
Db 301 AAIGGIPLLAGEYIIRCSEIPKLPVAVSLGGVWFLTAQDYVVIQAGQDVRLCLSGFRA 360

Qy 361 LDVPPAGPFWILGDVFLGYVAVFDRGDMKSSARVGLARPRGADLGHGETAQOFPFG 420
Db 361 LDIASPPVFWILGDVFLGYVAVFDRGDMKSGARVGLARPRGADLGRRTAQOYRG 420

RESULT 8
US-08-974-691-2
; Sequence 2, Application US/08974691
; Patent No. 6225103
; GENERAL INFORMATION:
; APPLICANT: Keolsch, Gerald
; APPLICANT: Lin, Xinli
; APPLICANT: Tang, Jordan
; TITLE OF INVENTION: Cloning and Characterization of Napsin
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 W. Peachtree
; STREET: St.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,691
; FILING DATE: 20-NOV-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,196
; FILING DATE: 20-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/046,126
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRP 166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-974-691-2

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Query Match      84.8%; Score 1897; DB 3; Length 451;
Best Local Similarity 86.0%; Pred. No. 3.6e-187;
Matches 361; Conservative 16; Mismatches 43; Indels 0; Gaps 0;

Qy 1 MSPPELLOPLLLPLLNVPESGATLIRPLHRVQPGRTTLNLRGWREPAELPKLGAPS 60
Db 1 MSPPELLOPLLLPLLNVPESGATLIRPLHRVQPGRTTLNLRGWREPAELPKLGAPS 60

Qy 61 PGDKPIFVPLSNRVDVQFGEIGLGTTPQNTFVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPASVPLSKFLDAQYFGEIGLGTTPQNTFVAFDTGSSNLWVPSRRCHFFSVPCWFHH 120

Qy 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAF 180

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Db 121 RFPNASSKPGSTKFAIQYGTGRVDGILSSEKLTIGGKAGSVIFGEALWESSLVTV 180
QY 181 AHFDGILGFPILSVGVRRPMDVLVEQGLDKPVSFYLNRPDPBPDGGELVLGGSDP 240
Db 181 SRPDGILGFPILSVGVRRPMDVLVEQGLDKPVSFYFNRPDPBPDGGELVLGGSDP 240
QY 241 AHYIPPLTFVPTVPAYQWQHMERVKVGPGLTCAKGAAILDGTSLITGPTTEIRALH 300
Db 241 AHYIPPLTFVPTVPAYQWQHMERVKVGSRLTCAQCAAILDGTPTVIVGPTTEIRALH 300
QY 301 AAGGIPLLAGEYIILCSEIPKLPAYSLFLGGVWENLTAHDYVIQTRNGVRLCLSGFOA 360
Db 301 AAGGIPLLAGEYIIRCSIEPKLPAYSLFLGGVWENLTAQDYVIQFAQGDVRLCLSGFRA 360
QY 361 LDVPPAGPFWILGDVFLGTVAVFDRGDMKSSARVGLARARTGADLGMGTGTAQAQFPG 420
Db 361 LDIASPPVFWILGDVFLGTVAVFDRGDMKSGARVGLARARPRGADLGRRETAQAQYRG 420

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RESULT 9

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US-09-705-448-3
; Sequence 3, Application US/09705448
; Patent No. 6432690
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Bruno, Sandra A.
; APPLICANT: Elsenboss, Laura A.
; APPLICANT: Fogliano, Michael
; APPLICANT: Cohan, Victoria L.
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN ASPARTIC PROTEASES
; FILE REFERENCE: PF-0458-1 CIP
; CURRENT APPLICATION NUMBER: US/09/705,448
; CURRENT FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 09/116,641
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/008,271
; PRIOR FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 433
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 322
; OTHER INFORMATION: 2435410, EOSINOT03
US-09-705-448-3

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```

Query Match 83.9%; Score 1877; DB 4; Length 433;
Best Local Similarity 85.2%; Pred. No. 4e-185;
Matches 358; Conservative 17; Mismatches 45; Indels 0; Gaps 0;

QY 1 MSPPLLOPLLLPLLLNVEPSGATLIRIPHRVQPGRTNLLRGWREPAPLPLKLGAPS 60
Db 1 MSPPLLLPLLLPLNVEPAGATLIRIPVQHPGRTNLLRGWKGAPLPLKLGAPS 60
QY 61 PGDKPIFVPLSNRYRDVQFGEIGLTPPONFTVAFTDGTSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPASPVLKFLDAQFGEIGLTPPONFTVAFTDGTSSNLWVPSRRCHFFSVPCWFHH 120
QY 121 RFDPKASSSQFQNGTKFAIQYGTGRVDGILSSEKLTIGGKAGSVIFGEALWESSLVTVAF 180
Db 121 RFPNASSKPGSTKFAIQYGTGRVDGILSSEKLTIGGKAGSVIFGEALWESSLVTV 180
QY 181 AHFDGILGFPILSVGVRRPMDVLVEQGLDKPVSFYLNRPDPBPDGGELVLGGSDP 240
Db 181 SRPDGILGFPILSVGVRRPMDVLVEQGLDKPVSFYFNRPDPBPDGGELVLGGSDP 240
QY 241 AHYIPPLTFVPTVPAYQWQHMERVKVGPGLTCAKGAAILDGTSLITGPTTEIRALH 300

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Db 241 AHYIPPLTFVPTVPAYQWQHMERVKVGSRLTCAQCAAILDGTPTVIVGPTTEIRALH 300
QY 301 AAGGIPLLAGEYIILCSEIPKLPAYSLFLGGVWENLTAHDYVIQTRNGVRLCLSGFOA 360
Db 301 AAGGIPLLAGEYIIRCSIEPKLPAYSLFLGGVWENLTAQDYVIQFAQGDVRLCLSGFRA 360
QY 361 LDVPPAGPFWILGDVFLGTVAVFDRGDMKSSARVGLARARTGADLGMGTGTAQAQFPG 420
Db 361 LDIASPPVFWILGDVFLGTVAVFDRGDMKSGARVGLARARPRGADLGRRETAQAQYRG 420

RESULT 10
US-08-974-691-3
; Sequence 3, Application US/08974691
; Patent No. 6225103
; GENERAL INFORMATION:
; APPLICANT: Keolsch, Gerald
; APPLICANT: Lin, Xinli
; APPLICANT: Tang, Jordan
; TITLE OF INVENTION: Cloning and Characterization of Napsin
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 W. Peachtree
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,691
; FILING DATE: 20-NOV-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,196
; FILING DATE: 20-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/046,126
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF 166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-691-3

Query Match 69.9%; Score 1564.5; DB 3; Length 419;
Best Local Similarity 70.5%; Pred. No. 6.8e-153;
Matches 297; Conservative 36; Mismatches 79; Indels 9; Gaps 3;

QY 7 LQPIILLPLL---NVPSGATLIRIPHRVQPGRTNLLRGWREPAPLPLKLGAPSPGD 63
Db 1 MSPILLLLCLLGNLEPEAKLRVPLQRIHLGRIILNPLNGWEQLAELSR--TSTSGG 58
QY 64 KPIFVPLSNRYRDVQFGEIGLTPPONFTVAFTDGTSSNLWVPSRRCHFFSVPCWLHHRFD 123
Db 59 NPSFVPLSKFWNTQYFGTIGLTPPONFTVAFTDGTSSNLWVPSRRCHFFSLACWFHHRFN 118
QY 124 PRASSSQFQNGTKFAIQYGTGRVDGILSSEKLTIGGKAGSVIFGEALWESSLVTVAF 183

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Db 119 PKASSFRDNGTKFALQYGTGRSLGSLSDNLTGIGHDFAVTFGEALWEPSLIFALAHF 178
QY 184 DGILGLGFPILSVGVRPPMDVLVEOGLLDKPVFSFYLNRDPEPPGCGELVLGGSDPAHY 243
Db 179 DGLILGFGFPLAVGGVQPPLDAMVEQGLLEKPVFSFYLNRDSEGSOGGELVLGGSDPAHY 238
QY 244 IPPLTFVPTVPAYWQIHMVRKVGGLTLCARCAAILDTGSLITGPTTEIRALHAAI 303
Db 239 VPPLTFIPVTIPAYWQVHMSVKVGTGLSLCAQCSAILDTGSLITGPTTEIRALNKAI 298
QY 304 GGIIPLAGEYIILCSBPKLPAVSLGGLWFWNLTAHDYVIQTRNGVRLCLSGFOALDV 363
Db 299 GGYFPLNGQYFIQCSKTPTLPPVSHLGGVWFWNLTAHDYVIQTRNGVRLCLSGFOALDI 358
QY 364 PPAGPFWLGDVFLGTYVAVFDRGDMKSSARVGLARTRGADLWGGETAQOAF---P 419
Db 359 PKPAGPLWILGDVFLGTYVAVFDRGDMKSSARVGLARTRGADLWGGETAQOAF---P 418
QY 420 G 420
Db 419 G 419

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RESULT 11
US-09-705-448-10
; Sequence 10, Application US/09705448
; Patent No. 6432690
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Bruno, Sandra A.
; APPLICANT: Eisenboss, Laura A.
; APPLICANT: Fogliano, Michael
; APPLICANT: Cohan, Victoria L.
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN ASPARTIC PROTEASES
; FILE REFERENCE: PF-0458-1 CIP
; CURRENT APPLICATION NUMBER: US/09/705,448
; CURRENT FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 09/116,641
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/008,271
; PRIOR FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 419
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
; FEATURE:
; OTHER INFORMATION: 1906810, GenBank
US-09-705-448-10

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Query Match 69.7%; Score 1560.5; DB 4; Length 419;
Best Local Similarity 70.3%; Pred. No. 1.8e-152;
Matches 296; Conservative 37; Mismatches 79; Indels 9; Gaps 3;

QY 7 LQPLLLLLPL---NVPSGATLIRIPHRVQGRRTLNLRGWREPAELPKLGAPSGD 63
Db 1 MSPILLLLCLLNLNLEPEERAKLRVPLQRIHLGHRILNPLNGWEQLAELSR--TSTSG 58

QY 64 KPFIPLSNTRDVQYFGEIGLGTTPQNTAFDTGSSNLWVPSRRCHFFSVPCWLHHRFD 123
Db 59 NPSEVPLSKFMTQYFGTIGLGTTPQNTAFDTGSSNLWVPSRRCHFFSVPCWLHHRFN 118

QY 124 PKASSSQANKTKFAIQGTGRVDGILSEDKLTGGIKGASVIFGEALWEPSLIFALAHF 183
Db 119 PKASSFRPNTKFAIQGTGRSLGSLSDNLTGIGHDFAVTFGEALWEPSLIFALAHF 178

QY 184 DGILGLGFPILSVGVRPPMDVLVEOGLLDKPVFSFYLNRDPEPPGCGELVLGGSDPAHY 243
Db 179 DGLILGFGFPLAVGGVQPPLDAMVEQGLLEKPVFSFYLNRDSEGSOGGELVLGGSDPAHY 238

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QY 244 IPPLTFVPTVPAYWQIHMVRKVGGLTLCARCAAILDTGSLITGPTTEIRALHAAI 303
Db 239 VPPLTFIPVTIPAYWQVHMSVKVGTGLSLCAQCSAILDTGSLITGPTTEIRALNKAI 298
QY 304 GGIIPLAGEYIILCSBPKLPAVSLGGLWFWNLTAHDYVIQTRNGVRLCLSGFOALDV 363
Db 299 GGYFPLNGQYFIQCSKTPTLPPVSHLGGVWFWNLTAHDYVIQTRNGVRLCLSGFOALDI 358
QY 364 PPAGPFWLGDVFLGTYVAVFDRGDMKSSARVGLARTRGADLWGGETAQOAF---P 419
Db 359 PKPAGPLWILGDVFLGTYVAVFDRGDMKSSARVGLARTRGADLWGGETAQOAF---P 418
QY 420 G 420
Db 419 G 419

RESULT 12
US-08-208-007A-12
; Sequence 12, Application US/08208007A
; Patent No. 5501969
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, ET AL.
; TITLE OF INVENTION: Human Osteoclast-Derived Cathepsin
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,007A
; FILING DATE: March 8, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5501969e
; FILING DATE: No. 5501969e
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TCPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-208-007A-12

```

```

Query Match 45.4%; Score 1015; DB 1; Length 412;
Best Local Similarity 46.9%; Pred. No. 3.5e-96;
Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;

QY 1 MSPPLIQLPLLLPLNLNLEPEERAKLRVPLQRIHLGHRILNPLNGWEQLAELSR--TSTSG 58
Db 1 MQPSLLPLALCLL---AAPASA-LVRIPHLKFTSIRRTMSEVSGSVEDLIAKGPVSKY 55

QY 55 KLGAAPSQDKPIFVPLSNTRDVQYFGEIGLGTTPQNTAFDTGSSNLWVPSRRCHFFSV 114
Db 56 SQAVPAVTEGPIEVLKXNYMDAQYIGIGITPPQCFVTFVDTGSSNLWVPSHCKLLDI 115

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Qy 115 PCWLHHRFDPKASSFOANGTKFAIYGTGRVDGILSSEDKLTI-----GGIKGA 163  
 Db 116 ACWIHHKYNDSKSTYKNGTSFDIHYGSGSLGYSQDTSVPCQSASSASALGGVKVE 175  
 Qy 164 SVIFGEALWEPSSLVFAFAHFDGILGFPILSVGVPPMDVLVEQGLLDPKPFVSYLNR 223  
 Db 176 RQVFEATKPGITFIAAKFDGILGMAYPRISVNNVLPVFDNLMOQKLVQDNIFSFYLSR 235  
 Qy 224 DPBEPDGGELVGGSDPAHYIPPLTFVPTVPAYWQIHMVRKVGPGITLCAKCAALID 283  
 Db 236 DPDAQPGGELMLGGTDSKYKGSLSYLVNTRKAYWQVHLDQVEVASGLTLCKEGCEAIVD 295  
 Qy 284 TGTSLITGPTTEIRALHAAIGGIPILAGEYIILCSEIPKLPKPAVSFLLGGVWFNLTADHYV 343  
 Db 296 TGTSLMWGPVDEVELOKAIGAVPLIQEYMPICEKVTSLPAILTLKLGKGYKLSPEYDT 355  
 Qy 344 IOTTRNGVRLCLSGFQALDVPDPAGPFWILGDVFLGTVAVFDGRDKMSSARVGLARA 401  
 Db 356 LKVSQAGKTLCLSGFMGMDDIPPSGFLMILGDVFIGRYTYTFDR-----DNNRVGFAEA 409

RESULT 13

US-08-974-691-4  
 ; Sequence 4, Application US/08974691  
 ; Patent No. 6225103  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keolsch, Gerald  
 ; APPLICANT: Lin, Xinli  
 ; APPLICANT: Tang, Jordan  
 ; TITLE OF INVENTION: Cloning and Characterization of Napsin  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Patrea L. Pabst  
 ; STREET: 2800 One Atlantic Center, 1201 W. Peachtree  
 ; CITY: Atlanta  
 ; STATE: GA  
 ; COUNTRY: USA  
 ; ZIP: 30309-3450  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/974,691  
 ; FILING DATE: 20-NOV-1997  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/031,196  
 ; FILING DATE: 20-NOV-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/046,126  
 ; FILING DATE: 09-MAY-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pabst, Patrea L.  
 ; REGISTRATION NUMBER: 31,284  
 ; REFERENCE/DOCKET NUMBER: OMR# 166  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 404-873-8794  
 ; TELEFAX: 404-873-8795  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 412 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; US-08-974-691-4

Query Match 45.4%; Score 1015; DB 3; Length 412;

Best Local Similarity 46.9%; Pred. No. 3.5e-96;  
 Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;  
 Qy 1 MSPPPLLOPLLLLPLLNVPSPGATLIRIPHRVQPGRRITNLLRGHRE-----PAELP 54  
 Db 1 MQPSSLLPLALCLL-----AAPASA-LVRIPLHKFTSIRRTMSEVGGSVEDLIAKGPVSKY 55  
 Qy 55 KLGAPSPGDKPIFVPLSNYRDVQYFGEIGLGTTPQNFVAFTDGTSSNLWVPSRRCHPFSV 114  
 Db 56 SQAVPAVTEGPPIPEVLKXNDQAQYGEIGIGTTPQCFTVVFDTGSSNLWVPSIHKLLDI 115  
 Qy 115 PCWLHHRFDPKASSFOANGTKFAIYGTGRVDGILSSEDKLTI-----GGIKGA 163  
 Db 116 ACWIHHKYNDSKSTYKNGTSFDIHYGSGSLGYSQDTSVPCQSASSASALGGVKVE 175  
 Qy 164 SVIFGEALWEPSSLVFAFAHFDGILGFPILSVGVPPMDVLVEQGLLDPKPFVSYLNR 223  
 Db 176 RQVFEATKPGITFIAAKFDGILGMAYPRISVNNVLPVFDNLMOQKLVQDNIFSFYLSR 235  
 Qy 224 DPBEPDGGELVGGSDPAHYIPPLTFVPTVPAYWQIHMVRKVGPGITLCAKCAALID 283  
 Db 236 DPDAQPGGELMLGGTDSKYKGSLSYLVNTRKAYWQVHLDQVEVASGLTLCKEGCEAIVD 295  
 Qy 284 TGTSLITGPTTEIRALHAAIGGIPILAGEYIILCSEIPKLPKPAVSFLLGGVWFNLTADHYV 343  
 Db 296 TGTSLMWGPVDEVELOKAIGAVPLIQEYMPICEKVTSLPAILTLKLGKGYKLSPEYDT 355  
 Qy 344 IOTTRNGVRLCLSGFQALDVPDPAGPFWILGDVFLGTVAVFDGRDKMSSARVGLARA 401  
 Db 356 LKVSQAGKTLCLSGFMGMDDIPPSGFLMILGDVFIGRYTYTFDR-----DNNRVGFAEA 409

RESULT 14

US-08-915-095A-12  
 ; Sequence 12, Application US/08915095A  
 ; Patent No. 6383793  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hastings, et al.  
 ; TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATHEPSIN  
 ; FILE REFERENCE: PF107D4  
 ; CURRENT APPLICATION NUMBER: US/08/915,095A  
 ; CURRENT FILING DATE: 1997-08-20  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 12  
 ; LENGTH: 412  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-08-915-095A-12

Query Match 45.4%; Score 1015; DB 4; Length 412;  
 Best Local Similarity 46.9%; Pred. No. 3.5e-96;  
 Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;  
 Qy 1 MSPPPLLOPLLLLPLLNVPSPGATLIRIPHRVQPGRRITNLLRGHRE-----PAELP 54  
 Db 1 MQPSSLLPLALCLL-----AAPASA-LVRIPLHKFTSIRRTMSEVGGSVEDLIAKGPVSKY 55  
 Qy 55 KLGAPSPGDKPIFVPLSNYRDVQYFGEIGLGTTPQNFVAFTDGTSSNLWVPSRRCHPFSV 114  
 Db 56 SQAVPAVTEGPPIPEVLKXNDQAQYGEIGIGTTPQCFTVVFDTGSSNLWVPSIHKLLDI 115  
 Qy 115 PCWLHHRFDPKASSFOANGTKFAIYGTGRVDGILSSEDKLTI-----GGIKGA 163  
 Db 116 ACWIHHKYNDSKSTYKNGTSFDIHYGSGSLGYSQDTSVPCQSASSASALGGVKVE 175  
 Qy 164 SVIFGEALWEPSSLVFAFAHFDGILGFPILSVGVPPMDVLVEQGLLDPKPFVSYLNR 223  
 Db 176 RQVFEATKPGITFIAAKFDGILGMAYPRISVNNVLPVFDNLMOQKLVQDNIFSFYLSR 235  
 Qy 224 DPBEPDGGELVGGSDPAHYIPPLTFVPTVPAYWQIHMVRKVGPGITLCAKCAALID 283  
 Db 236 DPDAQPGGELMLGGTDSKYKGSLSYLVNTRKAYWQVHLDQVEVASGLTLCKEGCEAIVD 295

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Qy 284 TGTSLITGPTBEIRALHAAIGGIPLLAGEYIILCSEIPKLPVSVFLGGVWFNLTAHDYV 343
Db 296 TGTSLMWGVPDVEVRELQKAGVPLIQGEYMWPCVKVSTLPAITIKLGKGYKLSPEYDT 355
Qy 344 IQTTRNGVRLCLSGFQALDVPVPPAGPFWILGDVFLGTGYVAVFDRGDMKSSARVGLARA 401
Db 356 LKVSQAGKTLCLSGFMGMNDIPPSGPLWILGDVFIGRYTYTVFDR----DNNRVGFAEA 409

RESULT 15
US-08-798-096-12
; Sequence 12, Application US/08798096
; Patent No. 6387682
; GENERAL INFORMATION:
; APPLICANT: Hastings, et al.
; TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATHEPSIN
; FILE REFERENCE: PF107D2
; CURRENT APPLICATION NUMBER: US/08/798,096
; CURRENT FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-798-096-12

Query Match 45.4%; Score 1015; DB 4; Length 412;
Best Local Similarity 46.9%; Pred. No. 3.5e-96;
Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;

Qy 1 MSPPPLQPLLLPLLNVPESGATLIRIPLHRYQPCRTLNLLRGWRE-----PAELP 54
Db 1 MQPSLLPLALCLL-----AAPASA-LVRIPLHKFTSIRRTMSEVGGSVEDLIAKGPVSKY 55
Qy 55 KLGAPSPGDKPIFVPLSNRYRDVQYFGEIGLGTPTPQNFVAFDTGSSNLWVPSRCHFFSV 114
Db 56 SQAVPAVTEGPIPEVLKNYMDAQYVGEIGIGTTPCCTVVFDTGSSNLWVPSIHKLLDI 115
Qy 115 PCWLHHRFPDKASSFPQANGTKFALIQYGTGRVDGLISEDKLT-----GGIKGA 163
Db 116 ACWTHHKYNSDKSTYVKNGTSPFDIHYGSSGLSYLSQDTVSPCQSASSASALGGVKVE 175
Qy 164 SVIFGEALWEPSLVFAFAHFDGILGLGFPILSVGVPRPPMDVLVEQGLDKPVFSFYLN 223
Db 176 RQVGEATKQGITFIAAKFDGILGMAYPRISVNNVLVFDNLMOQKLVQDNIFSYLSR 235
Qy 224 DPEEPDGGELVGGSDPAHYIPPLTFVPTVPYVQIHMERYKVGPGTLCAKCAAILD 283
Db 236 DPDAQPGGELMLGGTDSKYYKGSLSYLNVTWKAYVQVHLDOQVEVASGLTLCKEGCEAIVD 295
Qy 284 TGTSLITGPTBEIRALHAAIGGIPLLAGEYIILCSEIPKLPVSVFLGGVWFNLTAHDYV 343
Db 296 TGTSLMWGVPDVEVRELQKAGVPLIQGEYMWPCVKVSTLPAITIKLGKGYKLSPEYDT 355
Qy 344 IQTTRNGVRLCLSGFQALDVPVPPAGPFWILGDVFLGTGYVAVFDRGDMKSSARVGLARA 401
Db 356 LKVSQAGKTLCLSGFMGMNDIPPSGPLWILGDVFIGRYTYTVFDR----DNNRVGFAEA 409

Search completed: June 2, 2004, 20:23:16
Job time : 30.2707 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2004, 19:59:24 ; Search time 100.065 Seconds  
(without alignments)  
1185.931 Million cell updates/sec

Title: US-09-700-770-8

Perfect score: 2238

Sequence: 1 MSPPLIQPLLLPLINVE.....ARTRGADLGMGTAAQFPG 420

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A\_Geneseq\_29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2238	100.0	420	2	AAY06435 Human pro
2	2238	100.0	420	3	AAY44809 Human Asp
3	2238	100.0	420	3	AAY44457 Human lun
4	2232	99.7	420	2	AAW54878 Human nap
5	2232	99.7	420	6	AAE37358 Human nap
6	2232	99.7	433	5	AAO20497 Protein o
7	2069.5	92.5	395	2	AAW37958 Amino aci
8	1897	84.8	438	2	AAW57042 Human asp
9	1897	84.8	451	2	AAW54877 Human nap
10	1887	84.3	433	3	AAY44810 Human asp
11	1702.5	76.1	390	4	AAU09094 Novel hum
12	1678.5	75.0	449	2	AAW57043 Human asp
13	1560.5	69.7	419	3	AAY79177 Haematopo
14	1343	60.0	288	4	AAU23066 Novel hum
15	1328	59.3	262	4	AAW85539 Human sec
16	1328	59.3	262	5	ABG76585 Human sec
17	1328	59.3	262	5	ABG64720 Human alb
18	1179	52.7	285	3	AAW58332 Lung can
19	1050	46.9	212	4	AAW85560 Human sec
20	1050	46.9	212	5	ABG76606 Human sec
21	1050	46.9	212	5	ABG64722 Human alb
22	1037	46.3	410	4	AAE01672 Human gen
23	1037	46.3	410	5	ABG63963 Human alb
24	1037	46.3	410	6	ADA57122 Human sec
25	1037	46.3	410	6	ADA40983 Human sec

26	1037	46.3	410	6	ABR47867 Human sec
27	1037	46.3	410	7	ADC74257 Human sec
28	1015	45.4	412	2	AAR74207 Human dea
29	1015	45.4	412	2	AAW71369 Death ass
30	1015	45.4	412	2	AAW06478 Human tum
31	1015	45.4	412	3	AAY93685 Amino aci
32	1015	45.4	412	5	AAU72879 Human asp
33	1005.5	44.9	392	4	ABB58237 Drosophil
34	887	39.6	446	4	AAW63965 Amino aci
35	869	38.8	396	6	ABR48169 Human bla
36	869	38.8	396	6	ABU56634 Lung can
37	868	38.8	368	4	AAE01696 Human gen
38	868	38.8	368	5	ABG63960 Human alb
39	868	38.8	368	6	ADA57490 Human sec
40	868	38.8	368	6	ADA41368 Human sec
41	868	38.8	368	6	ABR48085 Human sec
42	868	38.8	368	7	ADC74513 Human col
43	868	38.8	404	4	AAW75543 Human col
44	841	37.6	215	4	AAW23663 Human EST
45	828.5	37.0	514	5	ABB07483 Theobroma

## ALIGNMENTS

RESULT 1

RAY06435

ID RAY06435 standard; protein; 420 AA.

XX AC

AC AC

XX 27-SEP-1999 (first entry)

DT XX

XX Human protease HUPM-4.

DE XX

XX Aspartic protease; human; HUPM-4; cell proliferation; cancer;

KW KW

KW immune disorder; inflammation; therapy.

XX OS

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..21

FT Protein /note= "putative signal peptide"

FT Modified-site 60

FT Modified-site 90

FT Active-site 96

FT Modified-site 106

FT Modified-site 133

FT Modified-site 143

FT Active-site 283

FT Region 309

FT Region 316

FT Modified-site 336

FT Modified-site 338

FT Modified-site 346

FT Modified-site 393

FT W09536550-A2.

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XX PD 22-JUL-1999.
XX PF 12-JAN-1999; 99WO-US000655.
XX PR 16-JAN-1998; 98US-00008271.
XX PA (INCY-) INCYTE PHARM INC.
XX Bandman O, Hillman JL, Yue H, Guegler KJ, Corley NC, Tang YT;
PI Shah P;
XX WPI: 1999-430616/36.
DR N-PSDB; AAX87152.
XX Novel human protease molecules useful in the treatment of developmental
PT disorders and/or cancers.
XX Claim 1; Page 72-73; 90pp; English.
XX The present sequence represents novel human protease HUPM-4, as deduced
CC from the consensus sequence (see AAX87152) of overlapping cDNA clones
CC obtained from various libraries. Northern analysis shows expression of
CC HUPM-4 in cardiovascular, haematopoietic, and male and female
CC reproductive cDNA libraries. Approximately 56% of these libraries are
CC associated with neoplastic disorders, 18% with inflammation and the
CC immune response, and 18% with trauma. The invention provides 12 new human
CC proteases, i.e. HUPM-1 to -12 (see AAX06432-43), and the polynucleotides
CC encoding them (see AAX87149-60). Also provided are vectors, host cells
CC and methods for producing HUPM polypeptides, as well as agonists and
CC antagonists of HUPM. Methods for treating or preventing cell
CC proliferative disorders and immune disorders using HUPM or HUPM
CC antagonists are claimed
XX SQ Sequence 420 AA;
Query Match 100.0%; Score 2238; DB 2; Length 420;
Best Local Similarity 100.0%; Pred No. 6.9e-203;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPPPLQLLLLLPLLNVEPSGATLIRPLHRVQGRRTNLLRGWRPAPLKLIGAPS 60
DB 1 MSPPPLQLLLLLPLLNVEPSGATLIRPLHRVQGRRTNLLRGWRPAPLKLIGAPS 60
QY 61 PGDKPIFVPLSNRYDVQYGEIGLTPPNFTVAEDTSSNLWVPSRRCHFFSVPCWLHH 120
DB 61 PGDKPIFVPLSNRYDVQYGEIGLTPPNFTVAEDTSSNLWVPSRRCHFFSVPCWLHH 120
QY 121 RDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEP SILVFAF 180
DB 121 RDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEP SILVFAF 180
QY 181 AHFDGILGFPILSVEGVRPMDVLVEOGLLDKPVFSFYLNDPDPGGEHLVGGSDP 240
DB 181 AHFDGILGFPILSVEGVRPMDVLVEOGLLDKPVFSFYLNDPDPGGEHLVGGSDP 240
QY 241 AHYIPPLTFVPVTVBAYWQIHMERVKVGPGLTICAKGCAILLDTGSLTGTPEETRALH 300
DB 241 AHYIPPLTFVPVTVBAYWQIHMERVKVGPGLTICAKGCAILLDTGSLTGTPEETRALH 300
QY 301 AAIIGIPLLAGIYIILCSEIKPLPAVSFLGGVWFNLTAHDYVIQITRNGVRLCLSGFQA 360
DB 301 AAIIGIPLLAGIYIILCSEIKPLPAVSFLGGVWFNLTAHDYVIQITRNGVRLCLSGFQA 360
QY 361 LDVPPAGPFWILGDVFLGTVAVFDRGDMKSSARVGLARPARTRGADLWGETAQOQFPG 420
DB 361 LDVPPAGPFWILGDVFLGTVAVFDRGDMKSSARVGLARPARTRGADLWGETAQOQFPG 420

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RESULT 2

AAY44809

ID AAY44809 standard; protein; 420 AA.

XX

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AC AAY44809;
XX 18-MAY-2000 (first entry)
XX Human Aspartic Protease-1 (NHAP-1).
XX Human; aspartic protease-1; NHAP-1; chromosome 19q13.3; anti-allergic;
KW immunosuppressive; cytostatic; antiasthmatic; anti-inflammatory; cancer;
KW antiarteriosclerotic; antithyroid; antibacterial; neuroprotective;
KW antidiabetic; anti-HIV; osteopathic; antiarthritic; treatment; cretinism;
KW endocrinological; hypogonadism; Sheehan syndrome; diabetes insipidus;
KW hypothyroidism; adenocarcinoma; leukaemia; immunological; amyloidosis;
KW acquired immune deficiency syndrome; AIDS; Addison's disease; arthritis;
KW osteoporosis; atherosclerosis; infection; respiratory; allergy; asthma;
KW emphysema; gene therapy; diagnosis.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Pep-ide 1..21
FT /label= Signal_peptide
FT /note= "Potential"
FT Protein 22..420
FT /label= Mature NHAP-1
FT /note= "Homologous to mouse aspartic protease-like
FT protein (GI 1906810)"
FT Modified-site 60
FT /note= "potential casein kinase II phosphorylation site"
FT Modified-site 90
FT /note= "Potential N-glycosylation site"
FT Active-site 96
FT /note= "Potential active site Asp residue characteristic
FT of aspartic proteases"
FT Modified-site 106
FT /note= "Potential protein kinase C phosphorylation site"
FT Modified-site 133
FT /note= "Potential N-glycosylation site"
FT Modified-site 143
FT /note= "Potential protein kinase C phosphorylation site"
FT Active-site 283
FT /note= "Potential active site Asp residue characteristic
FT of aspartic proteases"
FT Misc-difference 309
FT /note= "Potential Leucine zipper pattern start site"
FT Misc-difference 316
FT /note= "Potential Leucine zipper pattern start site"
FT Modified-site 336
FT /note= "Potential N-glycosylation site"
FT Modified-site 338
FT /note= "Potential casein kinase II phosphorylation site"
FT Modified-site 346
FT /note= "Potential protein kinase C phosphorylation site"
FT Binding-site 387..389
FT /note= "Potential cell attachment site"
FT Modified-site 393
FT /note= "Potential protein kinase C phosphorylation site"
XX WO200004137-A1.
PN 27-JAN-2000.
XX 15-JUL-1999; 99WO-US015988.
XX 16-JUL-1998; 98US-00116641.
XX (INCY-) INCYTE PHARM INC.
XX Xu H, Bruno SA, Elsenboss LA, Fogliano M, Cohan VL, Bandman O;
PI WPI: 2000-182413/16.
DR N-PSDB; AAX50231.
XX New human aspartic protease polypeptide useful for treating and detecting

```

PT endocrinological disorders e.g. hypogonadism, Sheehan syndrome and  
 XX diabetes insipidus.  
 XX  
 PS Disclosure; Fig 1; 83pp; English.  
 XX  
 CC The present sequence is human aspartic protease-1 (NHAP-1) encoded by  
 CC cDNA obtained from human lung cDNA library. NHAP-1 gene is located on  
 CC chromosome 19q13.3. NHAP has immunosuppressive, antiallergic, cytostatic,  
 CC antiasthmatic, antiinflammatory, antiarteriosclerotic, antithyroid,  
 CC antibacterial, neuroprotective, antidiabetic, anti-HIV, osteopathic and  
 CC antiarthritic activity. It is useful for treating and preventing  
 CC endocrinological disorders like hypogonadism, Sheehan syndrome, diabetes  
 CC insipidus, cretinism and hypothyroidism, cancers like adenocarcinoma and  
 CC leukaemia, immunological disorders like acquired immune deficiency  
 CC syndrome (AIDS), Addison's disease, amyloidosis, arthritis, osteoporosis,  
 CC atherosclerosis and microbial infections and respiratory disorders like  
 CC allergy, asthma and emphysema. NHAP polynucleotides can be used in gene  
 CC therapy and for diagnosis of disorders associated with expression of NHAP  
 XX  
 SQ Sequence 420 AA;

Query Match 100.0%; Score 2238; DB 3; Length 420;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-203;  
 Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSPPPQLQLLLPLLNVPSPGATLIRIPHRVQPGRRITNLLRGWREPAELPKLGAPS 60  
 DB 1 MSPPPQLQLLLPLLNVPSPGATLIRIPHRVQPGRRITNLLRGWREPAELPKLGAPS 60  
 QY 61 PGDKPIFVPLSNRDVQYFGEIGLTPPQNTFAFTGSSNLMWPSRRCHFFSVPCWLHH 120  
 DB 61 PGDKPIFVPLSNRDVQYFGEIGLTPPQNTFAFTGSSNLMWPSRRCHFFSVPCWLHH 120  
 QY 121 RFPKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPFLVFAF 180  
 DB 121 RFPKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPFLVFAF 180  
 QY 181 AHFDGILGLFPILSVGVRPPMDVLVEQGLLDPKVPFVFLNRDPDPDGELVLGSDP 240  
 DB 181 AHFDGILGLFPILSVGVRPPMDVLVEQGLLDPKVPFVFLNRDPDPDGELVLGSDP 240  
 QY 241 AHYIPPLTFVPTVPAYWQIHMERVKVGPGLTCAKGCALIDTGTSLITGPTTEIRALH 300  
 DB 241 AHYIPPLTFVPTVPAYWQIHMERVKVGPGLTCAKGCALIDTGTSLITGPTTEIRALH 300  
 QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTAHDYVIQTTNRGVRCLSGFOA 360  
 DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTAHDYVIQTTNRGVRCLSGFOA 360  
 QY 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARARTGADLGMGETAQAOFP 420  
 DB 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARARTGADLGMGETAQAOFP 420

RESULT 3  
 AAY44457  
 ID AAY44457 standard; protein; 420 AA.  
 AC AAY44457;  
 XX  
 XX 27-MAR-2000 (first entry)  
 XX Human lung specific gene protein Lngl105.  
 XX Lung Specific Gene; LSG; Lngl105; human; diagnostic marker; prognosticate;  
 XX lung cancer; diagnosis.  
 XX Homo sapiens.  
 OS  
 XX WO9960160-A1.  
 XX  
 XX 25-NOV-1999.  
 PD  
 XX

PF 12-MAY-1999; 99WO-US010344.  
 XX  
 PR 21-MAY-1998; 98US-0086212P.  
 XX  
 PA (DIAD-) DIADEXUS LLC.  
 XX  
 XX Yang F, Macina RA, Sun Y;  
 XX WPI; 2000-116320/10.  
 DR N-PEDB; AAZ29722.  
 XX  
 PT A new method for diagnosing, monitoring and staging lung cancer.  
 XX  
 PS Example 2; Page 37-38; 40pp; English.  
 XX  
 CC The present sequence is a lung specific gene (LSG) protein Lngl105 from  
 CC human clone ID 3107312. The LSG has high level of tissue specificity for  
 CC lungs and is overexpressed in cancerous tissues. The sequence serves as a  
 CC diagnostic marker for detecting, monitoring, staging and prognosticating  
 CC lung cancer. The diagnosis involves comparing levels of LSG in samples  
 CC obtained from patient and normal control  
 XX  
 SQ Sequence 420 AA;  
 Query Match 100.0%; Score 2238; DB 3; Length 420;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-203;  
 Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSPPPQLQLLLPLLNVPSPGATLIRIPHRVQPGRRITNLLRGWREPAELPKLGAPS 60  
 DB 1 MSPPPQLQLLLPLLNVPSPGATLIRIPHRVQPGRRITNLLRGWREPAELPKLGAPS 60  
 QY 61 PGDKPIFVPLSNRDVQYFGEIGLTPPQNTFAFTGSSNLMWPSRRCHFFSVPCWLHH 120  
 DB 61 PGDKPIFVPLSNRDVQYFGEIGLTPPQNTFAFTGSSNLMWPSRRCHFFSVPCWLHH 120  
 QY 121 RFPKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPFLVFAF 180  
 DB 121 RFPKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPFLVFAF 180  
 QY 181 AHFDGILGLFPILSVGVRPPMDVLVEQGLLDPKVPFVFLNRDPDPDGELVLGSDP 240  
 DB 181 AHFDGILGLFPILSVGVRPPMDVLVEQGLLDPKVPFVFLNRDPDPDGELVLGSDP 240  
 QY 241 AHYIPPLTFVPTVPAYWQIHMERVKVGPGLTCAKGCALIDTGTSLITGPTTEIRALH 300  
 DB 241 AHYIPPLTFVPTVPAYWQIHMERVKVGPGLTCAKGCALIDTGTSLITGPTTEIRALH 300  
 QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTAHDYVIQTTNRGVRCLSGFOA 360  
 DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTAHDYVIQTTNRGVRCLSGFOA 360  
 QY 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARARTGADLGMGETAQAOFP 420  
 DB 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARARTGADLGMGETAQAOFP 420

RESULT 4  
 AAW54878  
 ID AAW54878 standard; protein; 420 AA.  
 XX  
 XX AAW54878;  
 XX  
 XX 26-CCT-1998 (first entry)  
 XX Human napsin B protein.  
 XX Napsin B; splicing; clone; screening; human liver cDNA library;  
 XX aspartic protease; N-terminal; C-terminal; genomic clone; ss.  
 OS  
 XX Homo sapiens.  
 XX  
 XX WO9822597-A2.  
 XX



XX 28-MAY-1998.  
 XX 20-NOV-1997; 97WO-US021684.  
 XX 20-NOV-1996; 96US-0031196P.  
 XX 09-MAY-1997; 97US-0046126P.  
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 XX  
 XX Keolsch G, Lin X, Tang JUN;  
 XX WPI; 1998-312482/27.  
 XX N-PSDB; AAV27038.  
 XX  
 XX New isolated aspartic protease, napsin, from human liver - potentially  
 XX useful for, e.g. diagnosis and treatment of disease.  
 XX  
 XX Disclosure; Fig 4; 24pp; English.  
 XX  
 XX The present sequence represents the human napsin B protein, encoded by  
 XX the cDNA sequence given in AAV27038. The N-terminus of this cDNA was  
 XX obtained by splicing together isolated napsin cDNA clones, which had been  
 XX found by screening a human liver cDNA library, whereas the C-terminus was  
 XX obtained by using genomic clones. Napsin B is an aspartic protease which  
 XX was isolated from human liver  
 XX  
 XX Sequence 420 AA;

Query Match 99.7%; Score 2232; DB 2; Length 420;  
 Best Local Similarity 99.8%; Pred. No. 2.6e-202;  
 Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MSPPPLQLPLLLLPLLNVEPSGATLIRPLHRVQGRITLRLGWRPAPLPLKLGAPS 60  
 Db 1 MSPPPLQLPLLLLPLLNVEPSGATLIRPLHRVQGRITLRLGWRPAPLPLKLGAPS 60  
 QY 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAFTDGTSSNLWVPSRRCHFFSVPCWLHH 120  
 Db 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAFTDGTSSNLWVPSRRCHFFSVPCWLHH 120  
 QY 121 REDPKASSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAP 180  
 Db 121 REDPKASSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAP 180  
 QY 181 AHPDGILGLGFPILSVGVPRPMDVLVEQGLLDKPVFSFVFNLRDPREPDPGGELVLGSDP 240  
 Db 181 AHPDGILGLGFPILSVGVPRPMDVLVEQGLLDKPVFSFVFNLRDPREPDPGGELVLGSDP 240  
 QY 241 AHYIPPLTFVPTVPAYWQIHMERVKVGPGLTLCAGKCAAILDTGTSLLITGPTTEIRALH 300  
 Db 241 AHYIPPLTFVPTVPAYWQIHMERVKVGPGLTLCAGKCAAILDTGTSLLITGPTTEIRALH 300  
 QY 301 AATGGIPLLAGEVILLCSIEPKLPVNSFLLGGVWFNLTADHYVIOTRNGVRLCLSGFOA 360  
 Db 301 AATGGIPLLAGEVILLCSIEPKLPVNSFLLGGVWFNLTADHYVIOTRNGVRLCLSGFOA 360  
 QY 361 LDVPPAGPFWIIGDVLGTYVAVFDRGDMKSSARVGLARTRGADLNGETAGQAQFP 420  
 Db 361 LDVPPAGPFWIIGDVLGTYVAVFDRGDMKSSARVGLARTRGADLNGETAGQAQFP 420

RESULT 5  
 AAE37358  
 ID AAE37358 standard; protein; 420 AA.  
 XX  
 XX AAE37358;  
 XX  
 XX 27-AUG-2003 (first entry)  
 XX Human napsin A, 93804 protein.  
 XX  
 XX Human; cardiovascular disorder; coronary artery disease; bradycardia;

KW restenosis; cardiac hypertrophy; ischaemia reperfusion injury; angina;  
 KW arteriosclerosis; coronary artery ligation; rheumatic heart disease;  
 KW heart failure; hypertension; cardiomyopathy; myocardial infarction;  
 KW arterial inflammation; microembolism; atherosclerosis; endocarditis;  
 KW vascular heart disease; valvular disease; arrhythmia; gene therapy;  
 XX sinus node dysfunction; napsin A.  
 XX Homo sapiens.  
 XX WO2003039341-A2.  
 XX 15-MAY-2003.  
 XX 05-NOV-2002; 2002WO-US035538.  
 XX 05-NOV-2001; 2001US-0339582P.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Logan TJ, Chun M, Galvin KM;  
 XX WPI; 2003-441437/41.  
 XX N-PSDB; AAD56525.  
 XX  
 XX Treating a subject having a cardiovascular disorder, e.g. angina,  
 XX arrhythmia, or restenosis, comprises administering a 139, 258, 1261,  
 XX 1486, 2398, 2414, 7660, 8587, 10183, 10550, 12680, 17921, 32248, 60489 or  
 XX 93804 modulator.  
 XX  
 XX Disclosure; Page 123-124; 124pp; English.  
 XX  
 XX The invention relates to methods and compositions for treating a subject  
 XX having a cardiovascular disorder using 139, 258, 1261, 1486, 2398, 2414,  
 XX 7660, 8587, 10183, 10550, 12680, 17921, 32248, 60489 or 93804 modulator.  
 XX The invention is useful for treating a cardiovascular disorder, including  
 XX arteriosclerosis, atherosclerosis, vascular wall remodeling, inflammation,  
 XX cardiac hypertrophy, ischaemia reperfusion injury, arterial inflammation,  
 XX ventricular remodeling, rapid ventricular pacing, tachycardia, coronary  
 XX microembolism, bradycardia, pressure overload, aortic bending, coronary  
 XX artery ligation, valvular heart disease, valvular disease, including but  
 XX not limited to, valvular degeneration caused by calcification, rheumatic  
 XX heart disease, endocarditis, or complications of artificial valves;  
 XX atrial fibrillation, long-QT syndrome, congestive heart failure, sinus  
 XX node dysfunction, angina, heart failure, hypertension, atrial flutter,  
 XX atrial fibrillation, pericardial disease, including but not limited to  
 XX pericardial effusion and pericarditis, cardiomyopathies (e.g. dilated  
 XX cardiomyopathy or idiopathic cardiomyopathy), myocardial infarction,  
 XX coronary artery disease, coronary artery spasm, ischaemic disease,  
 XX arrhythmia, sudden cardiac death, and cardiovascular developmental  
 XX disorders. The invention is also useful in gene therapy. The present  
 XX sequence is human napsin A protein. This sequence is used to illustrate  
 XX the method of the invention

Sequence 420 AA;  
 Query Match 99.7%; Score 2232; DB 6; Length 420;  
 Best Local Similarity 99.8%; Pred. No. 2.6e-202;  
 Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MSPPPLQLPLLLLPLLNVEPSGATLIRPLHRVQGRITLRLGWRPAPLPLKLGAPS 60  
 Db 1 MSPPPLQLPLLLLPLLNVEPSGATLIRPLHRVQGRITLRLGWRPAPLPLKLGAPS 60  
 QY 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAFTDGTSSNLWVPSRRCHFFSVPCWLHH 120  
 Db 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAFTDGTSSNLWVPSRRCHFFSVPCWLHH 120  
 QY 121 REDPKASSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAP 180  
 Db 121 REDPKASSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAP 180  
 QY 181 AHPDGILGLGFPILSVGVPRPMDVLVEQGLLDKPVFSFVFNLRDPREPDPGGELVLGSDP 240  
 Db 181 AHPDGILGLGFPILSVGVPRPMDVLVEQGLLDKPVFSFVFNLRDPREPDPGGELVLGSDP 240

Db 181 AHFDGILGLGPPILSVGVRPMDVLVEQGLDKPVSFYLNRPDPDPDGELVLGGSDP 240  
 Qy 241 AHYIPPLTFVPTVPAYWQHMERVKVPGGLTLCAKCAALDGTSLITGPTTEIRALH 300  
 Db 241 AHYIPPLTFVPTVPAYWQHMERVKVPGGLTLCAKCAALDGTSLITGPTTEIRALH 300  
 Qy 301 AAGIGIPLLAGIYILCSEIIPKLPVAVSFLGGLGVWVFNLTADHYVITQTRNGVRLCLSGFQA 360  
 Db 301 AAGIGIPLLAGIYILCSEIIPKLPVAVSFLGGLGVWVFNLTADHYVITQTRNGVRLCLSGFQA 360  
 Qy 361 LDVPPAGPFWILGDVFLGTGVAVFDRGDMKSSARVGLARARTGADLGMGETAQAPPG 420  
 Db 361 LDVPPAGPFWILGDVFLGTGVAVFDRGDMKSSARVGLARARTGADLGMGETAQAPPG 420

RESULT 6

AAO20497  
 ID AAO20497 standard; protein; 433 AA.  
 XX AC AAO20497;

XX 27-JUN-2002 (first entry)

XX Protein of NAPI from aspartyl protease-related family.

XX Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;  
 KW amyloid precursor protein; tissue-specific expression control; human APP;  
 KW APP pathway modulator; gene therapy.

XX Homo sapiens.

XX WO200226820-A2.

XX 04-APR-2002.

XX 01-OCT-2001; 2001WO-EP011345.

XX 29-SEP-2000; 2000US-0236893P.

XX 14-JUN-2001; 2001US-0298309P.

XX (NOVS ) NOVARTIS AG.

XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Cohen D, Dengler UV, Finelli AL, Freuler F, Konsolaki M;

XX Reinhardt MWH, Zusan S;

XX WPI; 2002-315796/35.

XX N-PSDB; AAK99391.

XX New transgenic fly, containing DNA encoding an Abeta portion of human

XX APP, useful for identifying agents which modulate the APP pathway and

XX which can be used to treat Alzheimer's disease.

XX Example 4; Page 87-88; 129pp; English.

XX The invention relates to a transgenic fly whose genome comprises DNA  
 CC encoding a polypeptide having the Abeta portion of human amyloid  
 CC precursor protein (APP), fused to a signal sequence. The DNA sequence  
 CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in  
 CC the specification. The DNA sequence is operably linked to a tissue-  
 CC specific expression control sequence. Expression of the sequence gives  
 CC the fly an altered phenotype. The purpose of the invention is for  
 CC identifying agents that inhibit or promote the expression and/or function  
 CC of genes or encoded polypeptides which modify the APP pathway. The agent  
 CC is a compound, triple helix DNA, antisense oligonucleotide, double  
 CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used  
 CC to treat conditions such as Alzheimer's disease. The agent can be used as  
 CC an APP pathway modulator or in gene therapy. This sequence represents the  
 CC protein of the APP related NAPI from the aspartyl protease-related family

XX Sequence 433 AA;

Query Match 99.7%; Score 2232; DB 5; Length 433;

Best Local Similarity 99.8%; Pred. No. 2.7e-202;  
 Matches: 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 MSPPPLLOPLLLLLPLLNVPESGATLIRIPHRVQPGRTINLLRGHREPAELPKLGAPS 60  
 Db 14 MSPPLLOPLLLLLPLLNVPESGATLIRIPHRVQPGRTINLLRGHREPAELPKLGAPS 73  
 Qy 61 PGDKPIFVPLSNYRDVQYFGEIGLGTTPQNTFAFDTGSSNLWVPSRRCHFFSVPCWLHH 120  
 Db 74 PGDKPIFVPLSNYRDVQYFGEIGLGTTPQNTFAFDTGSSNLWVPSRRCHFFSVPCWLHH 133  
 Qy 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKNGASVIFGEALWEPSPAF 180  
 Db 134 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKNGASVIFGEALWEPSPAF 193  
 Qy 181 AHFDGILGLGPPILSVGVRPMDVLVEQGLDKPVSFYLNRPDPDPDGELVLGGSDP 240  
 Db 194 AHFDGILGLGPPILSVGVRPMDVLVEQGLDKPVSFYLNRPDPDPDGELVLGGSDP 253  
 Qy 241 AHYIPPLTFVPTVPAYWQHMERVKVPGGLTLCAKCAALDGTSLITGPTTEIRALH 300  
 Db 254 AHYIPPLTFVPTVPAYWQHMERVKVPGGLTLCAKCAALDGTSLITGPTTEIRALH 313  
 Qy 301 AAGIGIPLLAGIYILCSEIIPKLPVAVSFLGGLGVWVFNLTADHYVITQTRNGVRLCLSGFQA 360  
 Db 314 AAGIGIPLLAGIYILCSEIIPKLPVAVSFLGGLGVWVFNLTADHYVITQTRNGVRLCLSGFQA 373  
 Qy 361 LDVPPAGPFWILGDVFLGTGVAVFDRGDMKSSARVGLARARTGADLGMGETAQAPPG 420  
 Db 374 LDVPPAGPFWILGDVFLGTGVAVFDRGDMKSSARVGLARARTGADLGMGETAQAPPG 433

RESULT 7

AAW37958  
 ID AAW37958 standard; protein; 395 AA.  
 XX AC AAW37958;

XX 21-AUG-1998 (first entry)

XX Amino acid sequence of human cathepsin polypeptide-2.

XX Human cathepsin polypeptide-2; HCP-2; metatasis; antibody; agonist;  
 KW antagonists; tumour; arthritis; Alzheimer's disease; HCP-1;  
 KW Huntington's disease; mucopolidosis.

XX Homo sapiens.

XX WO9813484-A1.

XX 02-APR-1998.

XX 25-SEP-1997; 97WO-US017175.

XX 26-SEP-1996; 96US-00723938.

XX (INCY-) INCYTE PHARM INC.

XX Bandman O, Coleman R;

XX WPI; 1998-230698/20.

XX N-PSDB; AAV31665.

XX Human cathepsins and related nucleic acids, vectors and products - useful  
 PT for treatment and diagnosis of e.g. tumours, metastases, inflammation,  
 PT neurological disease etc.

XX Claim 15; Fig 5A-5D; 69pp; English.

XX This is the amino acid sequence of the human cathepsin polypeptide-2 (HCP  
 CC -2), which is involved in inflammation, metatasis and peptide/proenzyme  
 CC processing. HCP related products (e.g. antibodies, agonists, and  
 CC antagonists) are potentially useful for treating tumours, arthritis,

CC Alzheimer's and Huntington's diseases, and mucopolidosis. Fragments of  
 CC HCP-2 are useful diagnostically (to detect or quantify gene expression),  
 CC to monitor the effects of treatment and to map the corresponding genomic  
 CC sequences

XX Sequence 395 AA;

Query Match 92.5%; Score 2069.5; DB 2; Length 395;  
 Best Local Similarity 93.8%; Pred. No. 5.6e-187;  
 Matches 394; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

QY 1 MSPPLLOPLLLLLLLNVEPSGATLIRPLHRVQPGRRITNLRGWREPAELPKLGAPS 60  
 DB 1 MSPPLLOPLLLLLLLNVEPSGATLIRPLHRVQPGRRITNLRGWREPAELPKLGAPS 60

QY 61 PGDKPIFVPLSNRYRDVQVFEIGLTPPQNTFVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120  
 DB 61 PGDKPIFVPLSNRYRDVQVFEIGLTPPQNTFVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120

QY 121 RFDPKASSFOANGTKFAIQYGTGRVDGLSEDKLTIGIKGASVIFGEALWEPVSLVFAF 180  
 DB 121 RFDPKASSFOANGTKFAIQYGTGRVDGLSEDKLTIGIKGASVIFGEALWEPVSLVFAF 180

QY 181 AHFDGILGLGFPILSVGVRPMDVLEQGLDKPVSFYLNRPDPPEPDGGELVILGSDP 240  
 DB 181 AHFDGILGLGFPILSVGVRPMDVLEQGLDKPVSFYLNRPDPPEPDGGELVILGSDP 240

QY 241 AHYIPPLTFVPTVPAYQIHMVRKVGGLTLCAGCAAILDTGTSITGTTEIRALH 300  
 DB 241 AHYIPPLTFVPTVPAYQIHMVRKVGGLTLCAGCAAILDTGTSITGTTEIRALH 300

QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFLTAHDYVIOITTRNGVRLCLSGFQA 360  
 DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFLTAHDYVIOITTRNGVRLCLSGFQA 360

QY 361 LDVPPPPAGFWILGDVFLGTYYAVFDRGDMKSSARVGLARARTRGADLWGGETAQAPFG 420  
 DB 350 -----DVFLGTYYAVFDRGDMKSSARVGLARARTRGADLWGGETAQAPFG 395

RESULT 8  
 AAWS7042  
 ID AAWS7042 standard; protein; 438 AA.

XX AC AAWS7042;

XX DT 29-JUL-1998 (first entry)

XX DE Human aspartic protease SEQ ID NO:1.

XX KW Human; aspartic protease; EST; endothelin; serum amyloid A protein;  
 KW pro-opiomelanocortin prohormone.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 433 /note= "encoded by GAG"

FT Misc-difference 434 /note= "encoded by CTA"

FT Misc-difference 435 /note= "encoded by GCG"

FT Misc-difference 436 /note= "encoded by CTA"

FT Misc-difference 437 /note= "encoded by CTC"

FT Misc-difference 438 /note= "encoded by AGT"

XX WO9811236-A1.

XX PD 19-MAR-1998.

XX XX

PF 09-SEP-1997; 97WO-GB002426.  
 XX 11-SEP-1996; 96GB-00018966.  
 XX (SMK) SMITHKLINE BEECHAM PLC.  
 PA (UYWA-) UNIV WALES.

XX Powell D, Kay J, Hill J;

XX WPI. 1998-207396/18.

DR N-ESDB; AAV28623.

XX Human aspartic protease and related DNA - which may be involved in  
 PT processing of endothelin and pro-opiomelanocortin pro-hormone(s).

XX Claim 14; Page 20; 32pp; English.

CC The present sequence represents a human aspartic protease. The present  
 CC invention describes novel human aspartic proteases and also ESTs from  
 CC human cDNA libraries having partial DNA sequences which encodes an  
 CC aspartic protease. Compounds which inhibit aspartic protease, especially  
 CC antibodies can be used in therapy where needed. The protease can also be  
 CC used in therapy where needed. Important functions of aspartic proteases  
 CC are the processing of endothelin and pro-opiomelanocortin prohormones.  
 CC They may also be involved in the processing of serum amyloid A protein.

XX Sequence 438 AA;

Query Match 84.8%; Score 1897; DB 2; Length 438;

Best Local Similarity 86.0%; Pred. No. 1.4e-170;

Matches 361; Conservative 16; Mismatches 43; Indels 0; Gaps 0;

QY 1 MSPPLLOPLLLLLLLNVEPSGATLIRPLHRVQPGRRITNLRGWREPAELPKLGAPS 60

DB 1 MSPPLLOPLLLLLLLNVEPSGATLIRPLHRVQPGRRITNLRGWREPAELPKLGAPS 60

QY 61 PGDKPIFVPLSNRYRDVQVFEIGLTPPQNTFVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120

DB 61 PGDKPASVPLSKFLDAQYFGEIGLTPPQNTFVAFDTGSSNLWVPSRRCHFFSVPCWPHH 120

QY 121 RFDPKASSFOANGTKFAIQYGTGRVDGLSEDKLTIGIKGASVIFGEALWEPVSLVFAF 180

DB 121 RFPNASSSPKPSGKFAIQYGTGRVDGLSEDKLTIGIKGASVIFGEALWEPVSLVFAF 180

QY 181 AHFDGILGLGFPILSVGVRPMDVLEQGLDKPVSFYLNRPDPPEPDGGELVILGSDP 240

DB 181 SRPDGILGLGFPILSVGVRPMDVLEQGLDKPVSFYLNRPDPPEPDGGELVILGSDP 240

QY 241 AHYIPPLTFVPTVPAYQIHMVRKVGGLTLCAGCAAILDTGTSITGTTEIRALH 300

DB 241 AHYIPPLTFVPTVPAYQIHMVRKVGGLTLCAGCAAILDTGTSITGTTEIRALH 300

QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFLTAHDYVIOITTRNGVRLCLSGFQA 360

DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFLTAHDYVIOITTRNGVRLCLSGFQA 360

QY 361 LDVPPPPAGFWILGDVFLGTYYAVFDRGDMKSSARVGLARARTRGADLWGGETAQAPFG 420

DB 361 LDIASPPVPVWILGDVFLGAYTVVDRGDMKSGARVGLARARPRGADLGRRETAQAQYRG 420

RESULT 9

AAWS4877

ID AAWS4877 standard; protein; 451 AA.

XX AC AAWS4877;

XX DT 26-OCT-1998 (first entry)

XX DE Human napsin A protein.

XX Napsin A; splicing; clone; screening; human liver cDNA library;

KW aspartic protease; ss.

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XX OS Homo sapiens.
XX PN WO9822597-A2.
XX PD 28-MAY-1998.
XX PF 20-NOV-1997; 97WO-US021684.
XX PR 20-NOV-1996; 96US-0031196P.
XX FR 09-MAY-1997; 97US-0046128P.
XX FA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX PI Keolsch G, Lin X, Tang JUN;
XX DR WPI, 1998-312482/27.
XX DR N-PSDB; AAV27036.
XX PT New isolated aspartic protease, napsin, from human liver - potentially
XX PT useful for, e.g. diagnosis and treatment of disease.
XX PS Claim 3; Fig 1; 24pp; English.
XX CC The present sequence represents the human napsin A protein. The cDNA
XX CC sequence that produces this protein was obtained by splicing together
XX CC isolated napsin cDNA clones, which had been found by screening a human
XX CC liver cDNA library. Napsin A is an aspartic protease which was isolated
XX CC from human liver, however it has also been found to be present in other
XX CC human tissues
XX SQ Sequence 451 AA;

Query Match 84.8%; Score 1897; DB 2; Length 451;
Best Local Similarity 86.0%; Pred. No. 1.4e-170;
Matches 361; Conservative 16; Mismatches 43; Indels 0; Gaps 0;

QY 1 MSPPPPLLOPLLLPLLVNPSGATLIRIPHRVQPGRTNLLRGWREPAELPKLGAPS 60
DB 1 MSPPPPLLOPLLLPLLVNPSGATLIRIPHRVQPGRTNLLRGWREPAELPKLGAPS 60
QY 61 PGDKRIFVPLSNRYRVQVFEIGLGTTPQNFVAFDTGSSNLWVPSRCHFFSVPCWLHH 120
DB 61 PGDKPASVPLSKFLDAQVFEIGLGTTPQNFVAFDTGSSNLWVPSRCHFFSVPCWFHH 120
QY 121 RFDPKASSFQANGKFAIQGTGRVDGILSDKLTIGGIKASVIFGEALWEPSELVFAF 180
DB 121 RFNPNASSFPSPGKFAIQGTGRVDGILSDKLTIGGIKASVIFGEALWESSLVFTV 180
QY 181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKVFVSYLNRPDEEPDGGELVLGSGDP 240
DB 181 SRPDGILGLGFPILSVEGVRPPDLVLEQGLLDKVFVSYFNRPDEVADGGELVLGSGDP 240
QY 241 AHYIPPLTFVPTVPAYQIHMERYKVGSPGLTLCAGKCAALDTSITGPTTEIRALH 300
DB 241 AHYIPPLTFVPTVPAYQIHMERYKVGSRRLTLCAGCAALDTSITGPTTEIRALH 300
QY 301 AAIGGIPPLAGBYIILCSEIPKLPVAVSLIGGVWENLTAHDVYIQTTRNGVRLCLSGFOA 360
DB 301 AAIGGIPPLAGBYIIRCSSEIPKLPVAVSLIGGVWENLTAHDVYIQTTRNGVRLCLSGFRA 360
QY 361 LDVPPPPAGPFWLLGDVFLGTYVAVFDRGDMKSSARVGLARTRGADLGWGTAAQPPG 420
DB 361 LDIASPPVPVWLLGDVFLGTYVAVFDRGDMKSGARVGLARPRGADLGRETAAQYRG 420

RESULT 10
ID AAY44810
AC AAY44810 standard; protein; 433 AA.
XX AC AAY44810;
XX DT 18-MAY-2000 (first entry)

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XX DE Human Aspartic Protease-2 (NHAP-2).
XX KW Human; aspartic protease-2; NHAP-2; chromosome 19q13.3; antiallergic;
KW immunosuppressive; cytostatic; antidiabetic; antineoplastic; cancer;
KW antihypertensive; antithyroid; antibacterial; neuroprotective;
KW antidiabetic; anti-HIV; osteopathic; antirheumatic; treatment; creninism;
KW endocrinological; hypogonadism; Sheehan syndrome; diabetes insipidus;
KW hypothyroidism; adenocarcinoma; leukaemia; immunological; amyloidosis;
KW acquired immune deficiency syndrome; AIDS; Addison's disease; arthritis;
KW osteoporosis; atherosclerosis; infection; respiratory; allergy; asthma;
XX KW emphysema; gene therapy; diagnosis.
XX OS Homo sapiens.
XX FH Location/Qualifiers
XX FT 1. .21
XX FT /label= Signal_peptide
XX FT /note= "Potential"
XX FT 22. .433
XX FT /label= Mature NHAP-2
XX FT /note= "Homologous to mouse aspartic protease-like
XX FT protein (GI 1906810)"
XX FT 60
XX FT Modified-site
XX FT /note= "Potential casein kinase phosphorylation site"
XX FT 78
XX FT Modified-site
XX FT /note= "Potential Tyrosine kinase phosphorylation site"
XX FT 90
XX FT Modified-site
XX FT /note= "Potential N-glycosylation site"
XX FT 96
XX FT Active-site
XX FT /note= "Potential active site Asp residue characteristic
XX FT of aspartic proteases"
XX FT 106
XX FT Modified-site
XX FT /note= "Potential protein kinase C phosphorylation site"
XX FT 125
XX FT Modified-site
XX FT /note= "Potential N-glycosylation site"
XX FT 129
XX FT Modified-site
XX FT /note= "Potential protein kinase C phosphorylation site"
XX FT 143
XX FT Modified-site
XX FT /note= "Potential protein kinase C phosphorylation site"
XX FT 181
XX FT Modified-site
XX FT /note= "Potential casein kinase phosphorylation site"
XX FT 283
XX FT Active-site
XX FT /note= "Potential active site Asp residue characteristic
XX FT of aspartic proteases"
XX FT 336
XX FT Modified-site
XX FT /note= "Potential N-glycosylation site"
XX FT 338
XX FT Modified-site
XX FT /note= "Potential casein kinase phosphorylation site"
XX FT 383
XX FT Modified-site
XX FT /note= "Potential casein kinase phosphorylation site"
XX FT 387. .389
XX FT Binding-site
XX FT /note= "Potential cell attachment site"
XX FT 413
XX FT Modified-site
XX FT /note= "Potential cAMP-cGMP-dependent protein kinase
XX FT phosphorylation site"
XX PN WO200004137-A1.
XX PD 27-JAN-2000.
XX PF 15-JUL-1999; 99WO-US015988.
XX PR 16-JUL-1998; 98US-00116641.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Xu H, Bruno SA, Eisenboss LA, Fogliano M, Cohan VL, Bandman O;
XX DR WPI, 2000-182413/16.
XX DR N-PSDB; AAZ50232.
XX PT New human aspartic protease polypeptide useful for treating and detecting

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CC panic disorder, learning disabilities, amyotrophic lateral sclerosis,  
CC psychoses, autism, sleep disorders), immune system disorders (e.g.  
CC Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,  
CC central nervous system disorders (e.g. multiple sclerosis, ischaemic  
CC brain injury and/or stroke), infectious diseases, diabetes mellitus,  
CC immunological disorders (e.g. asthma, acquired immunodeficient syndrome  
CC (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,  
CC sepsis, acne, psoriasis and lupus erythematosus), neural system  
CC disorders, respiratory disorders, olfactory disorders and wound healing.  
XX The present sequence represents an NHP of the invention  
XX  
SQ Sequence 390 AA:  
  
Query Match 76.1%; Score 1702.5; DB 4; Length 390;  
Best Local Similarity 83.3%; Pred. No. 3e-152; Indels 45; Gaps 4;  
Matches 334; Conservative 7; Mismatches 15;  
  
QY 21 PSGATLIRPLHRVQPGRRTLNLRGWREPAELPKLGAPSPGDKPIFVPLSNRYDVQYFG 80  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
34 PSGATLIRPLHRVQPGRRTLNLRGWREPAELPKLGAPSPGDKPIFVPLSNYKG---- 88  
QY 81 EIGLTPPQNTVAFTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSSFQANGTKFAIQ 140  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
89 -----WLHHRFDPKASTP-SSQWDQFAIQ 111  
  
QY 141 YGTGRVDGILSEDKLTIGGIKASVIFGE-ALWEPISLVFAFAHFDGILGLGFPILSVGV 199  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
112 YGTGRVHGILSEDKLTIGGIKASVIFGELSGTQPL--RCPFDGILGLGFPILSVGV 169  
  
QY 200 RPPMDVIVEQGLDKPKVFSFYLNDRPEPDGELVLGSGDPANHYIPPLTPVPTVPAYWQ 259  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
170 RPPMDVIVEQGLDKPKVFSFYLNDRPEPDGELVLGSGDPANHYIPPLTPVPTVPAYWQ 229  
  
QY 260 IHMERVKVGLTLCAKGCRAALDGTSLTGTETETRAHRAAGGIPILAGEYIILCSE 319  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
230 IHMERVKVGLTLCAKGCRAALDGTSLTGTETETRAHRAAGGIPILAGEYIILCSE 289  
  
QY 320 IPKLPVPSFLLGGWFWNLTAHDYVVIQTRNGVRLCLSGFOALDVPPPPAGPFWILGDVFLG 379  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
290 IPKLPVPSFLLGGWFWNLTAHDYVVIQTRNGVRLCLSGFOALDVPPPPAGPFWILGDVFLG 349  
  
QY 380 TYVAVFDGRGDKMSARVGLARTRGADLWGNETAQAFPG 420  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
350 TYVAVFDGRGDKMSARVGLARTRGADLWGNETAQAFPG 390  
  
RESULT 12  
AAW57043  
AC AAW57043 standard; protein; 449 AA.  
XX  
XX AAW57043;  
XX  
DT 29-JUL-1998 (first entry)  
XX  
DE Human aspartic protease encoding cDNA SEQ ID NO:15.  
XX  
XX Human; aspartic protease; EST; endothelin; serum amyloid A protein;  
KW pro-Opimelanocortin prohormone.  
XX  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "encoded by NAA"  
FT Misc-difference 2 /note= "encoded by ANA"  
FT Misc-difference 410 /note= "encoded by TGA"  
FT Misc-difference 417 /note= "encoded by TGA"  
FT Misc-difference 427 /note= "encoded by TGN"  
FT Misc-difference 427 /note= "encoded by TGN"  
FT Misc-difference 433

FT Misc-difference 440 /note= "encoded by GMC"  
FT FT  
FT Misc-difference 442 /note= "encoded by TGA"  
FT FT  
FT Misc-difference 442 /note= "encoded by NGA"  
XX  
PN WO9811236-A1.  
XX  
PD 19-MAR-1998.  
XX  
XX 09-SEP-1997; 97WO-GB002426.  
XX  
XX 11-SEP-1996; 96GB-00018966.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (UYWA-) UNIV WALES.  
XX  
XX Powell D, Kay J, Hill J;  
PI  
XX WPI; 1998-207396/18.  
DR N-PSDB; AAV28624.  
XX  
XX Human aspartic protease and related DNA - which may be involved in  
PT processing of endothelin and pro-opimelanocortin pro-hormone(s).  
PT  
XX  
PS Claim 14; Page 23; 32pp; English.  
XX  
XX The present sequence represents a human aspartic protease. The present  
CC invention describes novel human aspartic proteases and also ESTs from  
CC human cDNA libraries having partial DNA sequences which encodes an  
CC aspartic protease. Compounds which inhibit aspartic protease, especially  
CC antibodies can be used in therapy where needed. The protease can also be  
CC used in therapy where needed. Important functions of aspartic proteases  
CC are the processing of endothelin and pro-opimelanocortin prohormones.  
CC They may also be involved in the processing of serum amyloid A protein  
XX  
SQ Sequence 449 AA;  
  
Query Match 75.0%; Score 1678.5; DB 2; Length 449;  
Best Local Similarity 81.1%; Pred. No. 6.8e-150;  
Matches 327; Conservative 18; Mismatches 55; Indels 3; Gaps 3;  
  
QY 9 PLILLLPLLNVEPSGATLIRPLHRVQPGRRTLNLRGWREPAELPKLGAPSPGDKPIFV 68  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
28 PSLLLLPLLNVEPAGATLIRPLRQVHGPGRRTNLLRGWGPALPKLGAPSPGDKPASV 87  
  
QY 69 PLSNRYDVQYFGEIGLTPPQNTVAFTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASS 128  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
88 PLSKFLDAQYFGEIGLTPPQNTVAFTGSSNLWVPSRRCHFFSVPCWFFHFRFNASS 147  
  
QY 129 SFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKASVIFGEALWEPISLVFAFAHFDGILG 188  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
148 SFKPSGTFKFAIQYGTGRVDGILSEDKLTIGGIKASVIFGEALWESSLVFTVSRPDGILG 207  
  
QY 189 LGPPIILSVGVRPPMDVIVEQGLDKPKVFSFYLNDRPEPDGELVLGSGDPANHYIPPLT 248  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
208 LGFPILSVGVRPPDVLVEQGLDKPKVFSFYFNDRPEVWNGSELVLGSGDPANHYIPLN 267  
  
QY 249 FVPVTPAYWQIEMERVKVGPGLTCAKGCRAALDGTGSL-ITGPTETETRAHRAAGGIP 307  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
268 FVPVTPAYWQIEMERVKVGPGRADSLCQGCRAALDGTGTLVITGPTETETRAHRAAGGIP 327  
  
QY 308 LLAGEYIILCSEIPKLPVPSFLLGGWFWNLTAHDYVVIQTRNG-VRLCLSGFOALDVPPP 366  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
328 LLAGEYIIRCSEIPKLPVPSLILGGWFWNLTAQDYVVIQTRKGDVRLCLSGFRALDIARA 387  
  
QY 367 AGPFWILGDVPLGYVAVFDGRGDKMSARVGLARTRGADLWG 409  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :  
388 EGPVWILGEVFWG-ICDRFDRGTXRANPSXLAGVALRGXPXG 429  
  
RESULT 13  
AAV79177

ID AAY79177 standard; protein; 419 AA.  
 XX AAY79177;  
 AC 19-JUN-2000 (first entry)  
 XX Haematopoietic stem cell specific protein.  
 DE Haematopoietic stem cell; immune system disorder; leukaemia;  
 XX antileukaemic; immunomodulator; therapy; mouse.  
 KW Mus musculus.  
 OS WO200011168-A2.  
 PN 02-MAR-2000.  
 PD 20-AUG-1999; 99WO-US019052.  
 XX 21-AUG-1998; 98US-00138132.  
 XX (OYPR-) UNIV PRINCETON.  
 PA Lemischka I, Moore K;  
 PI WPI; 2000-237650/20.  
 XX N-PSDB; AA294118.  
 DR Hematopoietic stem cell signaling proteins modulating replication and  
 XX differentiation for treating immune system disorders and leukemia.  
 PT Claim 21; Page 214-16; 256pp; English.  
 PS The present sequence is that of a mouse haematopoietic stem cell (HSC)  
 XX specific protein. It is an example of claimed HSC-specific proteins (see  
 CC AAY79176-93) predicted from novel isolated HSC-specific nucleic acids  
 CC (see AA294077-131). The HSCs are especially primitive HSCs (PHSCs) such  
 CC as umbilical cord cells, bone marrow cells and foetal liver cells. The  
 CC encoded proteins are growth factors, transcription factors, splicing  
 CC factors, capping factors, transport proteins, translation factors or  
 CC replication factors that modulate HSC activity, especially  
 CC differentiation or replication. The invention provides claimed methods:  
 CC for identifying PHSC-specific nucleic acids; for generating a stem  
 CC cell/progenitor cell from PHSCs; for identifying the presence of a PHSC  
 CC in a sample; for identifying the presence in a sample of a compound that  
 CC modulates HSC activity; for using such a compound to treat an immune  
 CC system condition, especially leukaemia; for introducing exogenous nucleic  
 CC acid into a HSC; and for ex vivo expansion of HSCs. Also claimed are  
 CC vectors, host cells, and an antibody that specifically binds a HSC-  
 CC specific protein  
 XX Sequence 419 AA;  
 SQ  
 Query Match 69.7%; Score 1560.5; DB 3; Length 419;  
 Best Local Similarity 70.3%; Pred. No. 9e-139;  
 Matches 296; Conservative 37; Mismatches 79; Indels 9; Gaps 3;  
 QY 7 LQPLLLPL--NVPSGATLIRILPHRVQGERLTLLRGWREPAELPKLGAPSGD 63  
 DB 1 MSPLLLLCLLGNLEPEAKLIRVPLQRIHLGHRINPLNGWEQLAELSR--TSTSGG 58  
 QY 64 KPFIPLSNYRDVQYFGEIGLTPPQNTVAFTDGTSSNLNVPSSRRCHFFSVPCWLHHRFD 123  
 DB 59 NPSEVPLSKPNTQYFTIGLTPPQNTVFTDGTSSNLNVPSTRCHFFSLACWFFHERFN 118  
 QY 124 PKASSSQANGTKFAIQYGTGRVDGILSEKLTGIGIKGASVIFGEALWEPFLVFAHAF 183  
 DB 119 PKASSFRPNTKFAIQYGTGRVSGILSQNLITGGIHDAFTVTFGEALWEPFLIFALAHF 178  
 QY 184 DGIILGLFPILSVGVPMPLVVEQGLDKPVSFYLNRDPEPDGELVLGGSDPAHY 243  
 DB 179 DGIILGLFPILVAGVPPPLDAMVEQGLLEKVPVSFYLNRDSEGDGELVLGGSDPAHY 238

QY 244 IPPLTFVPTVPAYQWQHMERVKVPGTLTCAKGCALIDTGTSLITGFTTEIRALHAAI 303  
 DB 239 VPPLTFVPTVPAYQWQWESVKVGTGLSLCAQGCALIDTGTSLITGFTTEIRALHAAI 298  
 QY 304 GGIPLLAGEYIILCSIEPKLPAVSPFLGGVWPNLTAHDYVITQTRNGVRLCLSGFOALDV 363  
 DB 299 GGYPLNGQYFTQCSKTPTLPPVSPHLLGGVWPNLTAHDYVITQTRNGVRLCLSGFOALDI 358  
 QY 364 PPAGPFWLGDVFLGTVVAVFDRGDKSSARVGLARARTRGADLWGGETAQAF---P 419  
 DB 359 PKPAGPLWLGVDVFLGTVVAVFDRGDKVNPVGLARARTRGADLWGGETAQAF---P 418  
 QY 420 G 420  
 DB 419 G 419  
 RESULT 14  
 AAU23066  
 ID AAU23066 standard; protein; 288 AA.  
 XX AAU23066;  
 AC AAU23066;  
 XX 18-DEC-2001 (first entry)  
 DT Novel human enzyme polypeptide #152.  
 DE Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;  
 XX ligase; hyperproliferative disorder; immunodeficiency disorder;  
 KW autoimmune disorder; neurological disorder; metabolic disorder;  
 KW inflammatory disorder; cardiovascular disorder; reproductive disorder;  
 KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;  
 KW nephrotropic; anticoagulant.  
 XX Homo sapiens.  
 OS WO200155301-A2.  
 PN 02-AUG-2001.  
 PD 17-JAN-2001; 2001WO-US001239.  
 XX 31-JAN-2000; 2000US-0179065P.  
 XX 04-FEB-2000; 2000US-0180628P.  
 XX 24-FEB-2000; 2000US-0184664P.  
 XX 02-MAR-2000; 2000US-0186350P.  
 XX 16-MAR-2000; 2000US-0189874P.  
 XX 17-MAR-2000; 2000US-0190076P.  
 XX 18-MAR-2000; 2000US-0198123P.  
 XX 19-MAY-2000; 2000US-0205515P.  
 XX 07-JUN-2000; 2000US-0209467P.  
 XX 28-JUN-2000; 2000US-0214886P.  
 XX 30-JUN-2000; 2000US-0215135P.  
 XX 07-JUL-2000; 2000US-0216647P.  
 XX 07-JUL-2000; 2000US-0216880P.  
 XX 11-JUL-2000; 2000US-0217487P.  
 XX 14-JUL-2000; 2000US-0218290P.  
 XX 26-JUL-2000; 2000US-0220963P.  
 XX 26-JUL-2000; 2000US-0220964P.  
 XX 14-AUG-2000; 2000US-0224518P.  
 XX 14-AUG-2000; 2000US-0224519P.  
 XX 14-AUG-2000; 2000US-0225213P.  
 XX 14-AUG-2000; 2000US-0225214P.  
 XX 14-AUG-2000; 2000US-0225266P.  
 XX 14-AUG-2000; 2000US-0225267P.  
 XX 14-AUG-2000; 2000US-0225268P.  
 XX 14-AUG-2000; 2000US-0225270P.  
 XX 14-AUG-2000; 2000US-0225447P.  
 XX 14-AUG-2000; 2000US-0225757P.  
 XX 14-AUG-2000; 2000US-0225758P.  
 XX 14-AUG-2000; 2000US-0225759P.  
 XX 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.  
 PR 22-AUG-2000; 2000US-0226686P.  
 PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-0227009P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
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 PR 12-SEP-2000; 2000US-0231968P.  
 PR 14-SEP-2000; 2000US-0232397P.  
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 PR 21-SEP-2000; 2000US-0234223P.  
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 PR 26-SEP-2000; 2000US-0235484P.  
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 PR 02-OCT-2000; 2000US-0236802P.  
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 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-0239935P.  
 PR 20-OCT-2000; 2000US-0239937P.  
 PR 20-OCT-2000; 2000US-0240960P.  
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 PR 08-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249207P.  
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 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 06-DEC-2000; 2000US-0256719P.  
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 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Barash SC, Ruben SM;  
 WP-; 2001-465566/50.  
 N-PSDB; AAS40936.  
 PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,  
 treating neural, immune system, muscular, reproductive, pulmonary,  
 cardiovascular, renal, proliferative disorders and cancerous diseases.  
 XX  
 Claim 11; SEQ ID NO 1062; 1180bp; English.  
 XX  
 CC The present invention relates to the isolation of novel human enzyme  
 polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences  
 encoding them. The enzyme polypeptides of the invention may comprise the  
 functional classes of oxidoreductases, transferases, hydrolases, lyases,  
 isomerases or ligases. The sequences of the invention are useful in the  
 diagnosis, treatment, prevention and/or prognosis of a wide range of  
 disorders including hyperproliferative disorders (e.g. cancer),  
 immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.  
 arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic  
 disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),  
 cardiovascular disorders (e.g. atherosclerosis), blood-related disorders  
 (e.g. haemophilia), reproductive disorders (e.g. infertility) and  
 infectious disorders (e.g. influenza). The polynucleotides of the  
 invention can also be used in gene therapy. AAU2915-AAU23814 represent  
 the novel human enzyme polypeptides of the invention. Note: The sequence  
 data for this patent did not form part of the printed specification, but  
 was obtained in electronic format directly from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 288 AA;

Query Match 60.0%; Score 1343; DB 4; Length 288;  
 Best Local Similarity 99.6%; Pred. No. 2.1e-118;  
 Matches 251; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MSPPPLQLLLLLPLLNVEPSGATLRPLHRVQGRITLLRWRPAPLPLKLGAPS 60  
 |||



Db 3 MSPPLLQPLLLPLLNVEPSGATLIRIPLHRVQPGRRILNLLRGWREPAELPKLGAPS 62  
 QY 61 PGDKPIFVPLSNYRDVQYFGEIGLGTTPQNTFAFDTGSSNLWVPSRCHFFSVPCWLHH 120  
 Db 63 PGDKPIFVPLSNYRDVQYFGEIGLGTTPQNTFAFDTGSSNLWVPSRCHFFSVPCWLHH 122  
 QY 121 RFDPKASSSFOANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180  
 Db 123 RFDPKASSSFOANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 182  
 QY 181 AHFDGILGLGFPILLSVEGVPRPMDVLVEQGLLDKPVFSFYLNRPDPDPGGELVLGGSDP 240  
 Db 183 AHFDGILGLGFPILLSVEGVPRPMDVLVEQGLLDKPVFSFYLNRPDPDPGGELVLGGSDP 242  
 QY 241 AHYIPPLTFVTV 252  
 Db 243 AHYIPPLTFVTV 254

RESULT 15  
 AAB85539  
 ID AAB85539 standard; protein; 262 AA.  
 XX  
 AC AAB85539;  
 XX  
 DT 25-SEP-2001 (first entry)  
 XX  
 DE Human secreted protein (clone Id HCRM212).  
 XX  
 KW Secreted protein; immunosuppressive; antiaarthritic; antirheumatic;  
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
 KW neotropic; neuroprotective; antibacterial; virucide; fungicide; human;  
 KW ophthalmological; gene therapy.  
 XX  
 OS Homo sapiens.

XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 231  
 FT /note= "Xaa can be any amino acid"  
 XX  
 XX WO200155430-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 XX 17-JAN-2001; 2001WO-US001431.  
 XX  
 XX 31-JAN-2000; 2000US-0179065P.  
 XX 04-FEB-2000; 2000US-0180628P.  
 XX 12-SEP-2000; 2000US-0231968P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;  
 PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;  
 PI Fiscella M, Ni J, Ruben SM, Barash SC;  
 XX  
 XX WPI; 2001-476220/51.  
 DR N-ESDB; AAH46949.  
 XX

17 isolated nucleic acid molecules encoding human secreted proteins, used to preventing, treating or ameliorating a medical condition.  
 Claim 11; Page 455-456; 482pp; English.

The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can also be used in diagnosing a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or

CC treated include autoimmune diseases e.g. rheumatoid arthritis,  
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
 CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.  
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and  
 CC ocular disorders e.g. corneal infection. The polypeptides can also be  
 CC used to aid wound healing and epithelial cell proliferation, to prevent  
 CC skin aging due to sunburn, to maintain organs before transplantation, for  
 CC supporting cell culture of primary tissues, to regenerate tissues and in  
 CC chemotaxis. The polypeptides can also be used as a food additive or  
 CC preservative to increase or decrease storage capabilities. The present  
 CC sequence represents a human secreted protein  
 XX

SQ Sequence 262 AA;  
 Query Match 59.3%; Score 1328; DB 4; Length 262;  
 Best Local Similarity 97.6%; Pred. No. 4.8e-117;  
 Matches 249; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MSPPLLQPLLLPLLNVEPSGATLIRIPLHRVQPGRRILNLLRGWREPAELPKLGAPS 60  
 Db 1 MSPPLLQPLLLPLLNVEPSGATLIRIPLHRVQPGRRILNLLRGWREPAELPKLGAPS 60  
 QY 61 PGDKPIFVPLSNYRDVQYFGEIGLGTTPQNTFAFDTGSSNLWVPSRCHFFSVPCWLHH 120  
 Db 61 PGDKPIFVPLSNYRDVQYFGEIGLGTTPQNTFAFDTGSSNLWVPSRCHFFSVPCWLHH 120  
 QY 121 RFDPKASSSFOANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180  
 Db 121 RFDPKASSSFOANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180  
 QY 181 AHFDGILGLGFPILLSVEGVPRPMDVLVEQGLLDKPVFSFYLNRPDPDPGGELVLGGSDP 240  
 Db 181 AHFDGILGLGFPILLSVEGVPRPMDVLVEQGLLDKPVFSFYLNRPDPDPGGELVLGGSDP 240  
 QY 241 AHYIPPLTFVTV 255  
 Db 241 AHYIPPSFFVVRSP 255

Search completed: June 2, 2004, 20:19:01  
 Job time : 103.065 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:07:29 ; Search time 14.9222 Seconds  
(without alignments)  
1966.411 Million cell updates/sec

Title: US-09-700-770-7

Perfect score: 459

Sequence: 1 MKLVTIFLLVTLTSLGYSAT.....LGPEASEAVKLLLEALSHLV 93

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_ivirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123.5	26.9	94	11 Q8CJC6	Q8cjc6 mus musculus
2	78.5	17.1	2109	8 Q32836	Q32836 pelargonium
3	76.5	16.7	1490	13 Q98TV5	Q98tv5 salmo salar
4	76.5	16.7	1519	13 Q9W750	Q9w750 salmo salar
5	75.5	16.4	1503	13 Q73677	Q73677 fundulus he
6	73.5	16.0	481	5 Q7YZ54	Q7yz54 cryptospori
7	73.5	16.0	1518	13 Q9IAR8	Q9iar8 salmo salar
8	73	15.9	630	16 Q836X7	Q836x7 enterococcu
9	71.5	15.6	542	17 Q8ZWX6	Q8zwy6 pyrobaculum
10	71	15.5	488	13 Q8W001	Q8w001 ictalurid p
11	70.5	15.4	1358	10 Q8W2P4	Q8w2p4 oryza sativ
12	70.5	15.4	1358	10 Q7XH05	Q7xh05 oryza sativ
13	70	15.3	106	10 Q9LVP3	Q9lvp3 arabidopsis
14	70	15.3	232	16 Q8XMB4	Q8xmb4 clostridium
15	70	15.3	603	10 Q7XRL3	Q7xrl3 oryza sativ
16	70	15.3	1502	10 Q9LYZ7	Q9lyz7 arabidopsis

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17 69.5 15.1 425 17 Q97W07
18 69.5 15.1 451 16 Q97W00
19 69.5 15.1 506 10 Q9M143
20 69.5 15.1 563 5 Q9N3Y4
21 69.5 15.1 568 16 Q97JD4
22 69.5 15.1 951 5 Q9W388
23 69 15.0 1000 11 Q8C488
24 69 15.0 1049 2 Q31100
25 69 15.0 1049 2 Q93PU4
26 68.5 14.9 208 10 Q9LRL3
27 68.5 14.9 231 2 Q9Z4I5
28 68.5 14.9 328 10 Q49847
29 68.5 14.9 335 10 Q65675
30 68.5 14.9 356 10 Q9M069
31 68.5 14.9 464 10 Q9M051
32 68.5 14.9 673 5 Q9W137
33 68.5 14.9 906 5 Q8I1J8
34 68.5 14.9 1284 12 Q8QMS9
35 68.5 14.9 1511 13 Q9I8E2
36 68 14.8 147 9 Q80190
37 68 14.8 239 16 Q66904
38 68 14.8 693 10 Q23122
39 68 14.8 1034 16 Q8AB07
40 67.5 14.7 288 16 Q98IG5
41 67.5 14.7 297 16 Q83NK5
42 67.5 14.7 297 16 Q83MX1
43 67.5 14.7 430 16 Q8PY8
44 67.5 14.7 485 10 Q8LPT2
45 67.5 14.7 512 10 Q9SY85
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#### ALIGNMENTS

RESULT 1

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Q8CJC6 PRELIMINARY; PRT; 94 AA.
AC Q8CJC6;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE UGRP2 type B.
GS SCG3A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2326074; PubMed=12438750;
RA Nimi T., Copeland N.G., Gilbert D.J., Jenkins N.A., Srisodhai A.,
RA Zimonjic D.B., Keck-Waggoner C.L., Popescu N.C., Kimura S.;
RT "Cloning, expression, and chromosomal localization of the mouse gene
RT (Scg3a1, alias Ugrp2) that encodes a member of the novel uteroglobin-
RT related protein gene family.";
RL Cytogenet. Genome Res. 97:120-127(2002).
DR EMBL; AF313457; AAN62328.1; --
DR MGD; MGI:1915912; Scgb3a1.
SQ SEQUENCE 94 AA; 9578 MW; 7C84B908A6365B59 CRC64;
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Query Match 26.9%; Score 123.5; DB 11; Length 94;

Best Local Similarity 43.1%; Pred. No. 2.5e-05;

Matches 31; Conservative 10; Mismatches 16; Indels 15; Gaps 2;

QY 30 PVDKLP-----LPLDNILPFMDPLKLLKTLGIVSEHLVEGLRKCVNELGPEA 78

DB 24 PVALAPAAEAAGAVGAPVSLPLSLA----ILRFILASMGIPLDPLIEGRKCVTELGPEA 79

QY 79 SEAVKKLEALS 90

DB 80 VGAVKSLGLVLT 91

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RESULT 2
Q32836 ID Q32836 PRELIMINARY; PRT; 2109 AA.
AC Q32836;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ORF2280.
OS Pelargonium hortorum (Common geranium).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Geraniales; Geraniaceae; Pelargonium.
OX NCBI_TaxID=4031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94363755; PubMed=8082181;
RA Downie S.R., Katz-Dowrie D.S., Wolfe K.H., Calie P.J., Palmer J.D.;
RT "Structure and evolution of the largest chloroplast gene (ORF2280):
RT internal plasticity and multiple gene loss during angiosperm
RT evolution.";
RL Curr. Genet. 25:367-378(1994).
DR EMBL; M83200; AAA73173.1; -.
DR PIR; T31352; T31352.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR008543; DUF825.
DR Pfam; PF05695; DUF825; 1.
DR SMART; SM00382; AAA; 2.
DR ATP-binding; Chloroplast.
KW SEQUENCE 2109 AA; 245645 MW; 948980477223DE8C CRC64;
SQ
Query Match 17.1%; Score 78.5; DB 8; Length 2109;
Best Local Similarity 24.0%; Pred. No. 31;
Matches 23; Conservative 16; Mismatches 24; Indels 33; Gaps 3;
QY 7 FLAVTSLCSYATAFELINKVPLFVDKLAFLPLDNLIPFM----- 46
DB 564 FLFVLRSFLYKSLPFLSLKLLSKL-FLLVSKVLPLLPFFVSCGNIPHRSE 622
QY 47 -----DPLKLLKTLGIVSHEVLGRLKCV 71
DB 623 IRIYELKGPVTPQCNPLLESIGLILHL-NKLKPLC 657
RESULT 3
Q98TY5 ID Q98TY5 PRELIMINARY; PRT; 1490 AA.
AC Q98TY5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator I.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX Chen J., Jacques C., Cutler C., Mercier B., Boeuf G., Ferec C.;
RT "Salmo salar cystic fibrosis transmembrane conductance regulator I.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AF319595; AA07405.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
Q98TY5 ID Q98TY5 PRELIMINARY; PRT; 1519 AA.
AC Q98TY5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator I.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX Chen J.M., Cutler C., Jacques C., Boeuf G., Denamur E., Lecointre G.,
RA Mercier B., Cramb G., Ferec C.;
RT "A Combined Analysis of the Cystic Fibrosis Transmembrane Conductance
RT Regulator: Implications for Structure and Disease Models.";
RL Mol. Biol. Evol. 18:1771-1788(2001).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AF155237; AAD38404.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABC_TM_transporter.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR005291; CAMP_cl_channel.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR TIGRFAMs; TIGR00953; 3a01202; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_2; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_2; 2.
DR ATP-binding; Transmembrane; Transport.
KW SEQUENCE 1519 AA; 171239 MW; F4A67DF2898240C CRC64;
SQ
Query Match 16.7%; Score 76.5; DB 13; Length 1490;
Best Local Similarity 36.4%; Pred. No. 35;
Matches 28; Conservative 10; Mismatches 24; Indels 15; Gaps 3;
QY 31 VDKLAPLPLDNLIPFMDP--LKLLKTLG-----ISVHVLGRLKCVNELGPEAS- 79
DB 1366 LSKARILLDDPSAFDLPITQLVRLKQLKQSFNSCTVILSEHRVPELLECCQSFMTIEGSS 1425
QY 80 ----EAVKLLLEALSHL 92
DB 1426 MKRYDSIQKLLNETSHL 1442
RESULT 4
Q9W750 ID Q9W750 PRELIMINARY; PRT; 1519 AA.
AC Q9W750;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator I.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396404; PubMed=11504857;
RA Chen J.M., Cutler C., Jacques C., Boeuf G., Denamur E., Lecointre G.,
RA Mercier B., Cramb G., Ferec C.;
RT "A Combined Analysis of the Cystic Fibrosis Transmembrane Conductance
RT Regulator: Implications for Structure and Disease Models.";
RL Mol. Biol. Evol. 18:1771-1788(2001).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AF155237; AAD38404.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABC_TM_transporter.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR005291; CAMP_cl_channel.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR TIGRFAMs; TIGR00953; 3a01202; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_2; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_2; 2.
DR ATP-binding; Transmembrane; Transport.
KW SEQUENCE 1519 AA; 171239 MW; F4A67DF2898240C CRC64;
SQ
Query Match 16.7%; Score 76.5; DB 13; Length 1519;
Best Local Similarity 36.4%; Pred. No. 36;
Matches 28; Conservative 10; Mismatches 24; Indels 15; Gaps 3;

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QY 31 VDKLAPLPLDNLFPMDP--LKLLKLTG-----ISVHLVGLRKCYNELGPEAS- 79
DB 1395 LSKARILLDPESAFDLPITQLVRLTKLQSFNSCTVILSEHRVPELLEQCSFLMIKSS 1454
QY 80 ----EAVKKLLEALSHL 92
DB 1455 MKRYDSIQKLNETHL 1471

RESULT 5
O73677
ID O73677 PRELIMINARY; PRT; 1503 AA.
AC O73677;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator.
GN CFTR.
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98191134; PubMed=9530103;
RA Singer T.D., Tucker S.J., Marshall W.S., Higgins C.F.;
RT "A divergent CFTR homologue: highly regulated salt transport in the
RT euryhaline teleost F. heteroclitus.";
RL Am. J. Physiol. 274:C715-C723(1998).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AF000271; AAC41271.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR001140; ABC TM transp.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR005291; cAMP-cl-channel.
DR Pfam; PF00664; ABC membrane; 2.
DR Pfam; PF00005; ABC tran; 2.
DR ProDom; PD000006; ABC transporter; 2.
DR SMART; SM00382; AAA; 2.
DR TIGRfams; TIGR00953; 3a01202; 1.
DR TIGRfams; TIGR01271; CFTR protein; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Transmembrane; Transport.
SQ SEQUENCE 1503 AA; 169250 MW; B95766EFA205920 CRC64;

Query Match 16.4%; Score 75.5; DB 13; Length 1503;
Best Local Similarity 35.1%; Pred. No. 45;
Matches 27; Conservative 14; Mismatches 21; Indels 15; Gaps 4;

QY 31 VDKLAPLPLDNLFPMDP--LKLLKLTG-----GISV--EHLVGLRKCYNELGPEAS- 79
DB 1379 LSKARILLDPSSYLDLPITQLVRLTKLQSFNSCTVILSEHKVPELLEQCSFLMIKSS 1439
QY 80 ----EAVKKLLEALSHL 92
DB 1439 VKSYDSIQKLNETHL 1455

RESULT 6
O7YZ54
ID O7YZ54 PRELIMINARY; PRT; 481 AA.
AC O7YZ54;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)

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DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Glutamine synthetase, probable.
GN IMB.677.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RA Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M.,
RA Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
RT "Integrated mapping, chromosomal sequencing and sequence analysis of
RT Cryptosporidium parvum.";
RL Genome Res 0:0-0(2003).
DR EMBL; BX538353; CAD98273.1; -.
SQ SEQUENCE 481 AA; 54314 MW; D7BEAB422FA18886 CRC64;

Query Match 16.0%; Score 73.5; DB 5; Length 481;
Best Local Similarity 24.4%; Pred. No. 23;
Matches 19; Conservative 18; Mismatches 32; Indels 9; Gaps 1;

QY 23 LINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISVHLVGLRKCYNELGPEAS--- 79
DB 186 LASRRPLQAYCAPYVDRLSLRSEILLELEENIGVTVEKHHVATCOHEIGVHCSTLV 245
QY 80 ----EAVKKLLEALSH 91
DB 246 QSADIVESIRYLKIGIAH 263

RESULT 7
O9IAR8
ID O9IAR8 PRELIMINARY; PRT; 1518 AA.
AC O9IAR8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator II.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396404; PubMed=11504857;
RA Chen J.M., Cutler C., Jacques C., Boeuf G., Denamur E., Lecointre G.,
RA Mercier B., Cramb G., Ferec C.;
RT "A Combined Analysis of the Cystic Fibrosis Transmembrane Conductance
RT Regulator: Implications for Structure and Disease Models.";
RL Mol. Biol. Evol. 18:1771-1788(2001).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AF161070; AAF37801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR001140; ABC TM transp.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR005291; cAMP-cl-channel.
DR Pfam; PF00664; ABC membrane; 2.
DR Pfam; PF00005; ABC tran; 2.
DR ProDom; PD000006; ABC transporter; 2.
DR SMART; SM00382; AAA; 2.
DR TIGRfams; TIGR00953; 3a01202; 1.
DR TIGRfams; TIGR01271; CFTR protein; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Transmembrane; Transport.
SQ SEQUENCE 1518 AA; 171136 MW; B3579B15820BA7F4 CRC64;

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Db 315 FLIVGVSLVLANAF-----DISKLTPIKELTSLRPLALSR-----PEG 358
Qy 67 LRKCVNELGPEASEAVKKLLEAL 89
Db 359 MRVVVNALFGAIPSGIVNVLLVCL 381

RESULT 11
Q8W2P4 PRELIMINARY; PRT; 1358 AA.
AC Q8W2P4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Putative aldehyde oxidase.
GN OSJNAA0087H07.7.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang R.A., Yu Y., Yang T.J., Nah G., Soderlund C., Chen M., Kim H.-R.,
RA Rambo T., Sasaki C., Henry D., Oates R., Simmons J.;
RT "Rice Genomic Sequence";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -I- COFACTOR: BINDS 1 2FE-2S CLUSTER (BY SIMILARITY).
DR EMBL; AC099733; AAL70116.1; -.
DR Gramene; Q8W2P4; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0004672; P:protein kinase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002888; 2Fe-2S bind.
DR InterPro; IPR006058; 2Fe2S fd BS.
DR InterPro; IPR008274; Aldoxan_dh bind.
DR InterPro; IPR000674; Aldoxan_dh hamm.
DR InterPro; IPR005107; CO deh flav C.
DR InterPro; IPR002346; dehydrog_molyb.
DR InterPro; IPR001041; Ferredoxin.
DR Pfam; PF01315; Ald_Xan_dh_C1.
DR Pfam; PF02738; Ald_Xan_dh_C2.
DR Pfam; PF03450; CO deh flav C; 1.
DR Pfam; PF00941; FAD binding_5; 1.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF01799; fer2.2; 1.
DR ProDom; PD186071; 2Fe-2S bind; 1.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
KW Iron; Iron-sulfur.
SQ SEQUENCE 1358 AA; 145453 MW; 75B3A692C75D537D CRC64;

Query Match 15.4%; Score 70.5; DB 10; Length 1358;
Best Local Similarity 27.9%; Pred. No. 1.4e+02;
Matches 24; Conservative 13; Mismatches 38; Indels 11; Gaps 3;

Qy 8 LLVTISL---CSYSATAFLINKVPLVDKLAFLPLDNLPLFMDPLKLLKTL-GISVVEHL 63
Db 407 LLISISIPDWCSDGITF-----ETFAAPRPFNGVSYNSAFLARSSLDAAAGSHL 459

Qy 64 VEGLRKCVNELGPEASEAVKKLLEAL 89
Db 460 IEDVRLAFGAFGSEHAIRASKVVEFL 485

RESULT 12
Q7XH05 PRELIMINARY; PRT; 1358 AA.
ID Q7XH05
Qy 315 FLIVGVSLVLANAF-----DISKLTPIKELTSLRPLALSR-----PEG 358
Qy 67 LRKCVNELGPEASEAVKKLLEAL 89
Db 359 MRVVVNALFGAIPSGIVNVLLVCL 381

Query Match 15.3%; Score 70; DB 10; Length 106;
Best Local Similarity 27.3%; Pred. No. 11;
Matches 21; Conservative 16; Mismatches 32; Indels 8; Gaps 2;

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AC Q7XH05;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Putative aldehyde oxidase.
GN OSJNAA0087H07.7.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10";
RL chromosome 10;
RL Science 300:1566-1569 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Bue.l C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017034; AAP52052.1; -.
SQ SEQUENCE 1358 AA; 145452 MW; 75B3A692C75D537D CRC64;

Query Match 15.4%; Score 70.5; DB 10; Length 1358;
Best Local Similarity 27.9%; Pred. No. 1.4e+02;
Matches 24; Conservative 13; Mismatches 38; Indels 11; Gaps 3;

Qy 8 LLVTISL---CSYSATAFLINKVPLVDKLAFLPLDNLPLFMDPLKLLKTL-GISVVEHL 63
Db 407 LLISISIPDWCSDGITF-----ETFAAPRPFNGVSYNSAFLARSSLDAAAGSHL 459

Qy 64 VEGLRKCVNELGPEASEAVKKLLEAL 89
Db 460 IEDVRLAFGAFGSEHAIRASKVVEFL 485

RESULT 13
Q9LVP3 PRELIMINARY; PRT; 106 AA.
ID Q9LVP3
AC Q9LVP3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Genomic DNA, chromosome 3, pl clone: MXE2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Columbia;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones";
RL DNA Res. 7:131-135 (2000).
DR EMBL; AB018121; BAB01992.1; -.
SQ SEQUENCE 106 AA; 11542 MW; 6AE232BFD4C5D0DD CRC64;

Query Match 15.3%; Score 70; DB 10; Length 106;
Best Local Similarity 27.3%; Pred. No. 11;
Matches 21; Conservative 16; Mismatches 32; Indels 8; Gaps 2;

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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:05:19 ; Search time 3.6175 Seconds  
(without alignments)  
1338.637 Million cell updates/sec

Title: US-09-700-770-7

Perfect score: 459

Sequence: 1 MKLVTFILVITSLCSYSAT.....IGPEASEAVKKLEALSHLV 93

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	459	100.0	93	1 UGR1_HUMAN	Q96pl1 homo sapien
2	326	71.0	139	1 UGR1_MOUSE	Q920h1 mus musculu
3	162.5	35.4	104	1 UGR2_MOUSE	Q920d7 mus musculu
4	159	34.6	104	1 UGR2_HUMAN	Q96qrl1 homo sapien
5	75.5	16.4	90	1 LPB2_HUMAN	Q95969 homo sapien
6	72	15.7	153	1 YF09_METJA	Q58304 methanococ
7	68.5	14.9	1284	1 ATL1_COWPX	P16602 cowpox viru
8	68	14.8	144	1 RPC_BPHFI	P06153 bacteriophage
9	67.5	14.7	764	1 SYFB_HELPJ	Q92kf8 helicobacte
10	67	14.6	95	1 PSC3_RAT	Q92780 rattus norv
11	67	14.6	445	1 MURD_RICPR	Q92dc2 rickettsia
12	66.5	14.5	91	1 UTER_HUMAN	P11684 homo sapien
13	66.5	14.5	395	1 NIFS_AZOCH	P23120 azotobacter
14	66.5	14.5	713	1 YD21_METJA	Q58717 methanococ
15	65.5	14.3	207	1 FRU_HIFPM	P35395 hypophthalm
16	65.5	14.3	844	1 CNA4_MOUSE	P54748 rattus norv
17	65	14.2	90	1 LPFA_HUMAN	Q95968 homo sapien
18	65	14.2	356	1 Y102_BACHD	Q9kgg3 bacillus ha
19	65	14.2	417	1 DCD4_VIBCH	Q9Kv17 vibrio chol
20	64.5	14.1	437	1 SAHH_PYRAE	Q82uq7 pyrobaculum
21	64.5	14.1	765	1 METE_LISIN	Q92ax9 listeria in
22	64	13.9	699	1 YQQA_CAEEL	Q92999 caenorhabdi
23	63.5	13.8	282	1 ZDHJ_HUMAN	Q8wvz1 homo sapien
24	63.5	13.8	432	1 HEM1_SYNXP	Q7u769 synechococ
25	63.5	13.8	749	1 PEX1_HUMAN	P78562 homo sapien
26	63.5	13.8	749	1 PEX_MOUSE	P70669 mus musculu
27	63.5	13.8	764	1 SYFB_HELPY	P56145 helicobacte
28	63	13.7	127	1 Y55B_MYCPN	P75047 mycoplasma
29	63	13.7	319	1 CAHC_SPIOL	P16016 spinacia ol
30	63	13.7	498	1 NDDD_ALCXX	P94212 alcaligenes
31	63	13.7	620	1 CHS5_SCHPO	Q92357 schizosacch
32	63	13.7	773	1 PAC2_PSESJ	P15558 pseudomonas
33	62.5	13.6	610	1 LEPA_BUCAI	P57348 buchnera ap

34	62.5	13.6	844	1 CNA4_MOUSE	O89084 mus musculu
35	62.5	13.6	886	1 CNA4_HUMAN	P27815 homo sapien
36	62	13.5	98	1 SZ10_HUMAN	P02778 homo sapien
37	62	13.5	239	1 RP35_BACAA	P26763 bacillus an
38	62	13.5	277	1 RS2_CHLPN	Q927k9 chlamydia p
39	62	13.5	342	1 Y755_METJA	Q58165 methanococ
40	62	13.5	363	1 LEU3_PICJA	O89791 pichia jadi
41	62	13.5	529	1 IMDH_MYCLE	Q49729 mycobacteri
42	62	13.5	2210	1 RRPO_LYCVA	P14240 lymphocytic
43	61.5	13.4	454	1 APY_SOLTU	P80595 solanum tub
44	61.5	13.4	562	1 Y55L_SYNY3	P74126 synechocyst
45	61.5	13.4	2434	1 ABC2_MOUSE	P41234 mus musculu

#### ALIGNMENTS

RESULT 1  
UGR1\_HUMAN STANDARD; PRT; 93 AA.  
AC Q96pl1,  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A member 2).  
DE member 2).  
GN SCG3A2 OR UGRP1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21539178; PubMed=11682631;  
RA Nilihi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., Kimura S.;  
RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor".  
RL Mol. Endocrinol. 15:2021-2036(2001).  
[2]  
SEQUENCE FROM N.A.  
TISSUE=Lung;  
MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Wang J., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., Morley K.C., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- SUBUNIT: Homodimer.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Highly expressed in lung.  
CC -!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.

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 CC -----

DR EMBL; AF313455; AAL26215.1; -  
 DR EMBL; BC024232; AAL24232.1; -  
 DR Genew; HGNC:18391; SCGB3A2.  
 DR MIM; 606531; -  
 KW Signal.

FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 93 UTEROGLOBIN-RELATED PROTEIN 1.  
 FT VARSPLIC 93 AA; 10161 MW; FBD4BFAC2BF3718 CRC64;  
 SQ SEQUENCE

Query Match 100.0%; Score 459; DB 1; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1e-39;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTLTISCSYSAFLINKVPLVDKLAFLPLDNLPLFMDPLKLLKLTGISV 60  
 DB 1 MKLVTFLLVTLTISCSYSAFLINKVPLVDKLAFLPLDNLPLFMDPLKLLKLTGISV 60

QY 61 EHLVEGLKCKVNLGPEASEAVKLLALSHLV 93  
 DB 61 EHLVEGLKCKVNLGPEASEAVKLLALSHLV 93

## RESULT 2

UGR1 MOUSE  
 ID UGR1\_MOUSE STANDARD; PRT; 139 AA.  
 AC Q920H1; Q920H2; Q920H3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A member 2).  
 DE member 2).  
 GN SCGB3A2 OR UGRP1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).  
 RC TISSUE=Lung;  
 RX MEDLINE=21539178; PubMed=11682631;  
 RA Kimura S.;  
 RA "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is  
 RT a novel lung-enriched downstream target gene for the T/EBP/NKX2.1  
 RT homeodomain transcription factor.";  
 RL Mol. Endocrinol. 15:2021-2036(2001).  
 CC -|- SUBUNIT: Homodimer.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=C;  
 CC IsoId=Q920H1-1; Sequence=Displayed;  
 CC Name=A;  
 CC IsoId=Q920H1-2; Sequence=VSP\_006727, VSP\_006728;  
 CC Name=B;  
 CC IsoId=Q920H1-3; Sequence=VSP\_006726;  
 CC -|- TISSUE SPECIFICITY: Highly expressed in lung.  
 CC -|- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.

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 CC -----

DR EMBL; AF274959; AAL25708.1; -  
 DR EMBL; AF274960; AAL25709.1; -

DR EMBL; AF274961; AAL25710.1; -  
 DR MGD; MGI:2153470; SCGB3A2.  
 DR GO; GO:0005576; C:extracellular; IDA.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR InterPro; IPR006038; Uteroglobin\_supf.  
 DR Pfam; PF01099; Uteroglobin; 1.  
 DR Signal; Alternative splicing.

FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 139 UTEROGLOBIN-RELATED PROTEIN 1.  
 FT VARSPLIC 107 139 VSVLFPMICAYPRDSKQTFAPFVRFQSKL -> EALS  
 FT FT HLV (in isoform B).  
 FT /FTId=VSP\_006726.

FT VARSPLIC 85 91 VIIICSY -> EALSHLV (in isoform A).  
 FT /FTId=VSP\_006727.  
 FT VARSPLIC 92 139 Missing (in isoform A).  
 FT /FTId=VSP\_006728.

SQ SEQUENCE 139 AA; 15431 MW; 8A2FB080B41E65E4 CRC64;

Query Match 71.0%; Score 326; DB 1; Length 139;  
 Best Local Similarity 77.9%; Pred. No. 4.3e-26;  
 Matches 67; Conservative 11; Mismatches 6; Indels 2; Gaps 2;

QY 1 MKLVTFLLVTLTISCSYSAFLINKVPLVDKLAFLPLDNLPLFMDPLKLLKLTGISV 60  
 DB 1 MKLVTFLLVTLTIGICYSATALLINLPV-VDKL-PVPLDDIIPSPDFLKMLLKLTGISV 58

QY 61 EHLVEGLKCKVNLGPEASEAVKLL 86  
 DB 59 EHLVTGLKCKVDLGPASEAVKLL 84

## RESULT 3

UGR2 MOUSE  
 ID UGR2\_MOUSE STANDARD; PRT; 104 AA.  
 AC Q920D7;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in  
 DE normal-1) (Secretoglobin family 3A member 1).  
 DE member 1).  
 GN SCGB3A1 OR UGRP2 OR HIN1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21396515; PubMed=11481438;  
 RA Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P.,  
 RA Kaelin C.M., Rhei E., Bosenberg M., Schnitt S., Marks J.R., Pagon Z.,  
 RA Belina D., Razumovic J., Polyak K.;  
 RA "HIN-1, a putative cytokine highly expressed in normal but not  
 RT cancerous mammary epithelial cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21539178; PubMed=11682631;  
 RA Nimmi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,  
 RA Kimura S.;  
 RA "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is  
 RT a novel lung-enriched downstream target gene for the T/EBP/NKX2.1  
 RT homeodomain transcription factor.";  
 RL Mol. Endocrinol. 15:2021-2036(2001).  
 CC -|- FUNCTION: Potential growth inhibitory cytokine.  
 CC -|- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -|- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.

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 CC -----

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

CC -----  
DR EMBL; AF313456; AAL26216.1; --  
DR MGD; MGI:1915912; Scgb3a1.  
KW Cytokine; Signal.  
FT SIGNAL 21 POTENTIAL.  
FT CHAIN 22 104 UTEROGLOBIN-RELATED PROTEIN 2.  
SQ SEQUENCE 104 AA; 10591 MW; D62F0E601FB57A6D CRC64;

Query Match 35.4%; Score 162.5; DB 1; Length 104;  
Best Local Similarity 40.0%; Pred. No. 1.1e-09;  
Matches 42; Conservative 17; Mismatches 27; Indels 19; Gaps 3;

QY 1 MKLVTFILVITSLCSYSATAFLINKVPL-----PVDKLP-----LPDNLDPF 45

Db 1 MKLTTTFLVLCVALLSDSGVAFPMDSIAKPAVEFVAALAPAAEAVAGAVPSLPLSLA-- 58

QY 46 MDPLKLLLTGLSVHEHLVEGLKVCNEIGPSEASAVKLLLEALS 90

Db 59 --ILRFILASMGIPLDPLIEGSRKCVTELGPFAVGAVKSLGLVLT 101

#### RESULT 4

UGR2\_HUMAN STANDARD; PRT; 104 AA.  
AC Q96QK1; Q96PL0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in normal-1) (Secretoglobin family 3A member 1).  
GN SCGB3A1 OR UGRP2 OR HIN1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21396515; PubMed=11481438;  
RA Krop I.B., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P., Kaelin C.M., Rhei E., Bosenberg M., Schnitt S., Marks J.R., Pagon Z., Beline D., Razumovic J., Polyak K.;  
RT "HIN-1, a putative cytokine highly expressed in normal but not cancerous mammary epithelial cells."  
RT Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21539178; PubMed=11682631;  
RA Nimri T., Keck-Weggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., Kimura S.;  
RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor."  
RL Mol. Endocrinol. 15:2021-2036(2001).  
CC -!- FUNCTION: Potential growth inhibitory cytokine.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Highly expressed in breast tissues. Absent in breast cancer cell lines.  
CC -!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.

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DR EMBL; AY040564; AAK82942.1; --  
DR EMBL; AF313458; AAL26217.1; --  
DR Genew; HGNC:18384; SCGB3A1.  
DR MIM; 606500; --

GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0005125; F:cytokine activity; NAS.  
DR GO; GO:0030308; P:negative regulation of cell growth; NAS.  
DR GO; GO:0042127; P:regulation of cell proliferation; NAS.  
KW Cytokine; Signal.  
FT SIGNAL 1 20 POTENTIAL.  
FT CHAIN 21 104 UTEROGLOBIN-RELATED PROTEIN 2.  
SQ CONFLICT 19 R -> A (IN REF. 2).  
SQ SEQUENCE 104 AA; 10185 MW; 1083873C8FAE8015 CRC64;

Query Match 34.6%; Score 159; DB 1; Length 104;  
Best Local Similarity 43.6%; Pred. No. 2.4e-09;  
Matches 44; Conservative 9; Mismatches 38; Indels 10; Gaps 2;

QY 1 MKLVTFILVITSLCSYSATAFLINKVPLPVDKLP-----PLDNLPEMDPLKL 51

Db 1 MKLAALLGLCVALLSCS-SARAEVLGSAKPAQVPAALSAEAAAGAGTLANPLGTLNPLKL 59

QY 52 LLKTTGISVEHLVEGLKVCNEIGPSEASAVKLLLEALS 92

Db 60 LLSSLGIPVNHLEGSQKCVAEIGPQAVGAVKALKALGAL 100

#### RESULT 5

LPFB\_HUMAN STANDARD; PRT; 90 AA.  
AC O95969;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lipophilin B precursor (Secretoglobin family 1D member 2).  
GN SCGB1D2 OR LPFB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99167354; PubMed=10066439;  
RA Zhao C., Nguyen T., Yusifov T., Glasgow B.J., Lehrer R.I.;  
RT "Lipophilins: human peptides homologous to rat prostatein."  
RL Biochem. Biophys. Res. Commun. 256:147-155(1999).  
CC -!- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS, MAY ALSO BIND ESTRAMUSTINE, A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER. MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.  
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION WAS FOUND IN SKELETAL MUSCLE. EXPRESSED AS WELL IN THYMUS, TRACHEA, KIDNEY, STEROID RESPONSIVE TISSUES (PROSTATE, TESTIS, UTERUS, BREAST AND OVARY), AND SALIVARY GLAND.  
CC -!- SIMILARITY: Belongs to the uteroglobin family. Lipophilin subfamily.

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DR EMBL; AJ224172; CAAL1864.1; --  
DR Genew; HGNC:18396; SCGB1D2.  
DR GO; GO:0005615; C:extracellular space; TAS.

DR InterPro; IPR000329; Uteroglobin subf.  
DR InterPro; IPR006038; Uteroglobin subf.  
DR Pfam; PF01039; Uteroglobin; 1.  
DR PRINTS; PR00486; UTEROGLOBIN.

KW SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 90 LIPOPHILIN B.  
SQ SEQUENCE 90 AA; 9925 MW; 17BB555ED035DIAF CRC64;

Query Match 16.4%; Score 75.5; DB 1; Length 90;



P06153; P15239;  
01-JAN-1988 (Rel. 06, Created)  
01-APR-1990 (Rel. 14, Last sequence update)  
15-MAR-2004 (Rel. 43, Last annotation update)  
Immunity repressor protein.  
Bacteriophage phi-105.  
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
Lambda-like viruses.  
NCBI\_TaxID=10717;  
[1]  
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
MEDLINE=86283656; PubMed=3135184;  
van Kaer L., Gansemans Y., van Montagu M., Dhaese P.;  
"Interaction of the Bacillus subtilis phage phi 105 repressor DNA: a  
genetic analysis";  
EMBO J. 7:859-866(1988).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=85297750; PubMed=2993999;  
Dhaese P., Seurinck J., de Smet B., van Montagu M.;  
"Nucleotide sequence and mutational analysis of an immunity repressor  
gene from Bacillus subtilis temperate phage phi 105";  
Nucleic Acids Res. 13:5441-5455(1985).  
[3]  
SEQUENCE FROM N.A.  
MEDLINE=86056972; PubMed=3934047;  
Cully D.F., Garro A.J.;  
"Nucleotide sequence of the immunity region of Bacillus subtilis  
bacteriophage phi 105: identification of the repressor gene and its  
mRNA and protein products";  
Gene 38:153-164(1985).  
-!- SIMILARITY: Contains 1 HTH cro/C1-type DNA-binding domain.  
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EMBL; X02799; CAA26567.1; ALT INIT.  
EMBL; M11920; AAA88396.1; -.  
PIR; A91579; RBPBP5.  
InterPro: IPR001387; HTH\_3.  
Pfam; PF01381; HTH\_3; 1.  
SMART; SM00530; HTH\_XRE; 1.  
PROSITE; PS0943; HTH\_CROCI; 1.  
Transcription regulation; Repressor; DNA-binding; Early protein.  
DOMAIN 7 61 HTH CRO/C1-TYPE.  
FT DNA BIND 18 37 H-T-H MOTIF (POTENTIAL).  
SQ SEQUENCE 144 AA; 16520 MW; EEED6EB3E4B34A1E CRC64;  
Query Match 14.8%; Score 68; DB 1; Length 144;  
Best Local Similarity 24.3%; Pred. No. 5.3;  
Matches 25; Conservative 13; Mismatches 33; Indels 32; Gaps 2;  
QY 23 LINKVPLPVDKLAFLDNLFPMDPLKLLKTLGIVSEHLV----- 64  
DB 21 LAEKANLSRYLADIERDYNPSLSLEAVAGALGQVSAIVGEETLIKEQAEYNSKEE 80  
QY 65 -----EGLRKVNELG-----PEASEAVKKLLEALSHLV 93  
DB 81 KOIAKMEERKLDKSDGLSFGSEPMQAEVSLMEAHIV 123  
RESULT 9  
ID -SYFB HELPJ STANDARD; PRT; 764 AA.  
AC Q9ZKF8;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)

Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)  
(Phenylalanine--tRNA ligase beta chain) (PHERS).  
PHE" OR JHP0979.  
Helicobacter pylori J99 (Campylobacter pylori J99).  
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
NCBI\_TaxID=85963;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=99120557; PubMed=9923682;  
Alm R.A., Lind L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,  
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,  
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,  
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
Trust T.J.;  
"Genomic sequence comparison of two unrelated isolates of the human  
gastric pathogen Helicobacter pylori";  
Nature 397:176-180(1999).  
-!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +  
diphosphate + L-phenylalanyl-tRNA(Phe).  
-!- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).  
-!- SUBUNIT: Tetramer of two alpha and two beta chains (By  
similarity).  
-!- SUBCELLULAR LOCATION: Cytoplasmic.  
-!- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain  
family. Subfamily 1.  
-!- SIMILARITY: Contains 1 tRNA-binding domain.  
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EMBL; AE001527; AAD06558.1; -.  
PIR; F71863; F71863.  
HAMAP; MF\_00283; -; 1.  
InterPro: IPR005146; B3\_4.  
InterPro: IPR005147; B5.  
InterPro: IPR005121; Fdx-AntiCB.  
InterPro: IPR008994; Nucleic\_acid\_08.  
InterPro: IPR004532; PheT\_bact.  
InterPro: IPR002547; tRNA\_bind.  
Pfam; PF03483; B3\_4; 1.  
Pfam; PF03484; B5; 1.  
Pfam; PF03147; FDX-ACB; 1.  
Pfam; PF01588; tRNA\_bind; 1.  
TIGRFAMs; TIGR00472; PheT\_bact; 1.  
PROSITE; PS50886; TRBD; 1.  
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
Metal-binding; Magnesium; RNA-binding; tRNA-binding;  
Complete proteome.  
KW Complete proteome.  
FT DOMAIN 38 148 TRNA-BINDING.  
FT METAL 433 433 MAGNESIUM (BY SIMILARITY).  
FT METAL 439 439 MAGNESIUM (VIA CARBONYL OXYGEN)  
(BY SIMILARITY).  
FT METAL 442 442 MAGNESIUM (BY SIMILARITY).  
FT METAL 443 443 MAGNESIUM (BY SIMILARITY).  
SQ SEQUENCE 764 AA; 85154 MW; 70BDAFD202FED425 CRC64;  
Query Match 14.7%; Score 67.5; DB 1; Length 764;  
Best Local Similarity 38.0%; Pred. No. 33;  
Matches 27; Conservative 10; Mismatches 27; Indels 7; Gaps 4;  
QY 20 TAPLINVPLPVDKLAFLDNLFPMDPLKLLKTLGIVSEHLVVEGLVKVCNELGPFA 78  
DB 690 TAFSKIKKAL---KDAQIPNLSEILP-LDIFKESGNTIALSRVCVTHSLKTLND--EEV 743  
QY 79 SEAVKKLLEAL 89  
DB 744 NSAVOKALEIL 754



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CC -----  
 DR EMBL; AJ235271; CAA14867.1; -;  
 DR PIR; A71699; A71699.  
 DR HSSP; P14900; 1UAG.  
 DR HAMAP; MF\_00639; -; 1.  
 DR InterPro; IPR000713; Mur\_ligase.  
 DR InterPro; IPR004101; Mur\_ligase\_C.  
 DR InterPro; IPR005762; MurD.  
 DR Pfam; PF01225; Mur\_ligase; 1.  
 DR Pfam; PF02875; Mur\_ligase\_C; 1.  
 DR TIGRfams; TIGR01087; murD; 1.  
 DR Peptidoglycan synthesis; Cell wall; Cell division; Ligase;  
 KW ATP-binding; Complete proteome  
 FT NP\_BIND 111 117 ATP (POTENTIAL).  
 SQ SEQUENCE 445 AA; 50129 MW; B9CCCF7437FB7AA6 CRC64;

Query Match 14.6%; Score 67; DB 1; Length 445;  
 Best Local Similarity 32.0%; Pred. No. 22;  
 Matches 31; Conservative 12; Mismatches 24; Indels 30; Gaps 6;

QY 6 IFLLV-----TISCSYSATAFLINKVLPVVKIAPLPLDNLIPMPDLKLLKTLGISVE 61  
 DB 221 IFVLLKQDSIKLIPSVTKILKNGISIVDDKIH-----DNDLYKFLN---KNL----- 268  
 QY 62 HLVEGLKCKNELGPSEAV-----KKLLEALS 90  
 DB 269 ---QGLHCNEN---IAASYAVAKIIGLESKKILESIS 299

## RESULT 12

UTER\_HUMAN STANDARD; PRT; 91 AA.  
 AC F11684; Q9UCM2; Q9UCM4;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Clara cell phospholipid-binding protein precursor (CCBP) (Clara cells  
 DE 10 kDa secretory protein) (CC10) (Uteroglobin) (Urine protein 1)  
 DE (UPI).  
 GN SCGB1A1 OR UGB OR CC10 OR CCSP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=89000784; PubMed=3167058;  
 RA Singh G., Katyal S.L., Brown W.E., Phillips S., Kennedy A.L.,  
 RA Anthony J., Squeglia N.;  
 RT "Amino-acid and cDNA nucleotide sequences of human Clara cell 10 kDa  
 RT protein.";  
 RL Biochim. Biophys. Acta 950:329-337(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=95250987; PubMed=7733299;  
 RA Hay J.G., Daniel C., Chu C., Crystal R.G.;  
 RT "Human CC10 gene expression in airway epithelium and subchromosomal  
 RT locus suggest linkage to airway disease.";  
 RL Am. J. Physiol. 268:L565-L575(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=92388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP SEQUENCE OF 1-18 FROM N.A.  
 RX MEDLINE=93250776; PubMed=1284526;  
 RA Wolf M., Klug J., Hackenberg R., Gessler M., Grzeschik K.-H.,  
 RA Beato M., Suske G.;  
 RT "Human CC10, the homologue of rabbit uteroglobin: genomic cloning,  
 RT chromosomal localization and expression in endometrial cell lines.";  
 RL Hum. Mol. Genet. 1:371-378(1992).  
 RN [5]  
 RP SEQUENCE OF 22-74.  
 RC TISSUE=Urine;  
 RX MEDLINE=93016476; PubMed=1400743;  
 RA Okutani R., Itoh Y., Hirata H., Kasahara T., Mukaida N., Kawai T.;  
 RT "Simple and high-yield purification of urine protein 1 using  
 RT immunoaffinity chromatography: evidence for the identity of urine  
 RT protein 1 and human Clara cell 10-kilodalton protein.";  
 RL J. Chromatogr. A 577:25-35(1992).  
 RN [6]  
 RP SEQUENCE OF 22-45.  
 RC TISSUE=Urine;  
 RX MEDLINE=93009001; PubMed=1395029;  
 RA Bernard A., Roels H., Lauwerys R., Witters R., Gielens C.,  
 RA Soumillon A., Van Damme J., De Ley M.;  
 RT "Human urinary protein 1: evidence for identity with the Clara cell  
 RT protein and occurrence in respiratory tract and urogenital  
 RT secretions.";  
 RL Clin. Chim. Acta 207:239-249(1992).  
 RN [7]  
 RP SEQUENCE OF 22-33.  
 RX MEDLINE=21648993; PubMed=11788998;  
 RA Chafouri B., Stahlbom B., Tagesson C., Lindahl M.;  
 RT "Newly identified proteins in human nasal lavage fluid from  
 RT non-smokers and smokers using two-dimensional gel electrophoresis and  
 RT peptide mass fingerprinting.";  
 RL Proteomics 2:112-120(2002).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=95393197; PubMed=7664082;  
 RA Um and T.C., Swaminathan S., Singh G., Warty V., Furey W.,  
 RA Pletcher J., Sax M.;  
 RT "Structure of a human Clara cell phospholipid-binding protein-ligand  
 RT complex at 1.9-A resolution.";  
 RL Nat. Struct. Biol. 1:538-545(1994).  
 CC -1- FUNCTION: BINDS PHOSPHATIDYLCHOLINE, PHOSPHATIDYLINOSITOL,  
 CC POLYCHLORINATED BIPHENYLS (PCB) AND WEAKLY PROGESTERONE, POTENT  
 CC INHIBITOR OF PHOSPHOLIPASE A2.  
 CC -1- SUBUNIT: Homodimer; antiparallel disulfide-linked.  
 CC -1- TISSUE SPECIFICITY: Clara cells (nonciliated cells of the  
 CC surface epithelium of the pulmonary airways).  
 CC -1- SIMILARITY: Belongs to the uteroglobin family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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DR EMBL; X13197; CAA31584.1; -
DR EMBL; U01101; AAA81885.1; -
DR EMBL; U01102; AAA18297.1; -
DR EMBL; BC004481; AAH04481.1; -
DR EMBL; X59875; CAA42532.1; -
DR PIR; JS0036; JS0036.
DR PIR; S26651; S26651.
DR HSSP; P02779; IUTG.
DR GENE; HGNC:12523; SCGB1A1.
DR MIM; 192020; -.
DR GO; GO:0007566; P:embryo implantation; TAS.
DR InterPro; IPR006039; Uterogl.
DR InterPro; IPR003628; Uteroglobn subf.
DR InterPro; IPR000329; Uteroglobln subf.
DR InterPro; IPR006038; Uteroglobln subf.
DR Pfam; PF01099; Uteroglobln; 1.
DR PRINTS; PR00486; UTEROGLOBIN.
DR ProDom; PD012475; Uteroglobn_sub; 1.
DR SMART; SM00096; UTG; 1.
DR PROSITE; PS00403; UTEROGLOBIN 1; 1.
DR PROSITE; PS00404; UTEROGLOBIN 2; 1.
DR Phospholipase A2 inhibitor; Signal; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 91
FT DISULFID 24 24
FT DISULFID 90 90
FT VARIANT 56 56
FT VARIANT 68 68
FT CONFLICT 24 24
FT SEQUENCE 91 AA; 9994 MW; FE65ACA678F12ABD CRC64;
Query Match 14.5%; Score 66.5; DB 1; Length 91;
Best Local Similarity 25.2%; Pred. No. 4.7;
Matches 26; Conservative 16; Mismatches 30; Indels 31; Gaps 3;
QY 1 MKLAVTFLVLTISCSYATFLINKVLPVDPKLAFLPDLNLPFMDPLKLLKLTGISV 60
DB 1 MKLAVTFLVLTALCCSSASA-----EICP-----SFQVETLLMDTFSY 42
QY 61 EHLVE-----GLRKCYNELGPSEAVKLLKLEALS 90
DB 43 EAMELFSPQDMREAGALQKLVDTLPQKPRESIKLMKIA 85
RESULT 13
NIFS AZOCH STANDARD; PRT; 395 AA.
AC P23120;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Cysteine desulfurase (EC 4.4.1.-) (Nitrogenase metalloclusters biosynthesis protein nifs).
GN NIFS.
OS Azotobacter chroococcum mcd 1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91358323; PubMed=1885524;
RA Evans D.J., Jones R., Woodley P.R., Wilborn J.R., Robson R.L.;
RT "Nucleotide sequence and genetic analysis of the Azotobacter chroococcum nifUSVWZM gene cluster, including a new gene (nifp) which encodes a serine acetyltransferase."
RL J. Bacteriol. 173:5457-5469(1991).
CC -!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM CYSTEINE TO PRODUCE ALANINE. SEEMS TO PARTICIPATE IN THE BIOSYNTHESIS OF THE NITROGENASE METALLOCLUSTERS BY PROVIDING THE INORGANIC SULFUR REQUIRED FOR THE FE-S CORE FORMATION (BY SIMILARITY).
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CC -!- COPACTOR: Pyridoxal phosphate (By similarity).
CC -!- SURUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent aminotransferases. Nifs/iscs subfamily.
CC
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CC
CC EMBL; M60090; AAA22160.1; -.
DR PIR; B43706; B43706.
DR InterPro; IPR000192; Aminotrans_V.
DR Pfam; PF00266; aminotran_5; 1. CLASS 5; 1.
DR PROSITE; PS00595; AA_TRANSF_P; Pyridoxal phosphate.
KW Nitrogen fixation; Lyase; Pyridoxal phosphate.
FT INIT MET 0 BY SIMILARITY.
FT BINDING 198 198 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT ACT SITE 318 318 BY SIMILARITY.
FT SEQUENCE 395 AA; 43165 MW; 909F70995B312BDA CRC64;
Query Match 14.5%; Score 66.5; DB 1; Length 395;
Best Local Similarity 28.9%; Pred. No. 21;
Matches 24; Conservative 18; Mismatches 30; Indels 11; Gaps 4;
QY 12 ISLCSYSAT-AFLINKVLPVDPKLAFLPDLNLPFMDPLKLLKLTGISVE---HLVSG 66
DB 100 LSLCDYLASEGYTVHK--LPVDKKGRLDLDHVASLINDVAVSVWANNETGLFPVEE 157
QY 67 LRKCYNELG-----PEASEAVKKL 85
DB 158 MAAMADEAGIMFTDAVQVRKL 180
RESULT 14
YD21 METJA STANDARD; PRT; 713 AA.
ID YD21 METJA
AC Q58717;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical protein MJ1321.
GN MJ1321.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RC MEDLINE=9637999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hirst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii."
RN [1]
RP SEQUENCE FROM N.A.
RX Science 273:1058-1073(1996).
CC -!- SIMILARITY: Contains 1 Pwi domain.
CC
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:14:10 ; Search time 6.33063 Seconds

(without alignments)  
1413.099 Million cell updates/sec

Title: US-09-700-770-7

Perfect score: 459

Sequence: 1 MKLVTFILVTLISCSYSAT.....LGPEASEAVKKLLEALSHLV 93

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78.5	17.1	2109	T31352	hypothetical prote
2	72	15.7	153	D64488	hypothetical prote
3	70	15.3	1502	T48309	hypothetical prote
4	69.5	15.1	425	H90415	hypothetical prote
5	69.5	15.1	451	A96920	probable ABC trans
6	69.5	15.1	506	F85016	probable RING zinc
7	69.5	15.1	568	E97066	membrane associate
8	68.5	14.9	335	T05268	hypothetical prote
9	68.5	14.9	356	D85406	hypothetical prote
10	68.5	14.9	464	T47710	glucuronosyl trans
11	68.5	14.9	1284	1 RWVZAI	A-type inclusion p
12	68	14.8	147	1 RBPFF5	immunity repressor
13	68	14.8	239	D70359	conserved hypothet
14	68	14.8	693	C86364	hypothetical prote
15	67.5	14.7	512	A86238	protein F14N23.31
16	67.5	14.7	566	AD0816	nitrate/nitrite se
17	67.5	14.7	764	F71863	phenylalanine-tRNA
18	67	14.6	95	1 BORT3	prostatic steroid-
19	67	14.6	445	A71699	UDP-n-acetylmuram
20	66.5	14.5	91	1 JS0036	Clara cell 10K pro
21	66.5	14.5	128	T15017	hypothetical prote
22	66.5	14.5	396	B43706	nitrogenase cofact
23	66.5	14.5	713	H64464	hypothetical prote
24	66	14.4	379	F96565	hypothetical prote
25	66	14.4	415	G75179	hypothetical prote
26	66	14.4	793	C83260	hypothetical prote
27	66	14.4	983	H72510	probable ribonucle
28	66	14.4	2471	T42977	large tegument pro
29	65.5	14.3	192	F72559	hypothetical prote

30	65.5	14.3	207	2	S21965	prolactin - silver
31	65.5	14.3	390	2	AH0052	Hmr protein [limpo
32	65.5	14.3	844	2	I53865	phosphodiesterase
33	65	14.2	308	1	S53538	protein kinase [EC
34	65	14.2	356	2	P83662	creatine kinase BH
35	65	14.2	384	2	T37111	probable transcrip
36	65	14.2	417	2	F82360	diaminopimelate de
37	65	14.2	704	2	H82381	toxin secretion AT
38	65	14.2	964	2	H89582	protein K07E3.6 [i
39	64.5	14.1	715	2	C70174	methyl-accepting c
40	64.5	14.1	765	2	AD1656	cobalamin-independ
41	64.5	14.1	1120	2	H84449	protein F54D8.1 [i
42	64	13.9	432	2	T20929	hypothetical prote
43	64	13.9	667	2	G89978	DNA ligase [import
44	64	13.9	699	2	T15920	hypothetical prote
45	63.5	13.8	116	2	H90622	NADH dehydrogenase

ALIGNMENTS

RESULT 1

T31352

hypothetical protein - Pelargonium x hortorum

C:Species: Pelargonium x hortorum

C>Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 02-Sep-2000

C:Accession: T31352

R:Downie, S.R.; Katz-Downie, D.S.; Wolfe, K.H.; Calie, P.J.; Palmer, J.D.

Curr. Genet. 25, 367-378, 1994

A:Title: Structure and evolution of the largest chloroplast gene (ORF2280) : internal reference number: Z21012; MUID:94363755; PMID:8082181

A:Accession: T31352

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2109 <DOW>

A:Cross-references: EMBL:M83200; NID:G468913; PID:G468914; PIDN:AAA73173.1

Query Match 17.1%; Score 78.5; DB 2; Length 2109;

Best Local Similarity 24.0%; Pred. No. 13;

Matches 23; Conservative 16; Mismatches 24; Indels 33; Gaps 3;

QY 7 FLVTVISCSYSATAFINKVLPVDKLAFLPLDNLIFPM----- 46

DB 564 FLVTVISCSYSATAFINKVLPVDKLAFLPLDNLIFPM----- 46

QY 47 -----DPLKLLKTLGISVEHLVEGLRKCV 71

DB 623 IRIYELKGTVPQPCNPFLLESIGLQILHL-NKLKPL 657

RESULT 2

D64488

hypothetical protein M11509 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000

C:Accession: D64488

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blal

; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,

raon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: D64488

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-153 <BUL>

A:Cross-references: GB:U67592; GB:L77117; NID:G2826425; PIDN:AAB99534.1; PID:G1500391

C:Genetics:

A:Map position: FOR1482026-1482487

Query Match 15.7%; Score 72; DB 2; Length 153;

Best Local Similarity 28.8%; Pred. No. 3.8;



membrane associated chemotaxis sensory transducer protein (MSP domain and HAMP domain)  
C:Species: Clostridium acetobutylicum  
C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C:Accession: E97066  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: E97066  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-568 <KUR>  
A:Cross-references: GB:AS001437; PIDN:AAK79320.1; PID:gl5024285; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC1352

Query Match 15.1%; Score 69.5; DB 2; Length 568;  
Best Local Similarity 24.8%; Pred. No. 27;  
Matches 27; Conservative 19; Mismatches 44; Indels 19; Gaps 3;

QY 1 MKLVTFILVITSLGYSATAPFLINKVPLVDKL---APLPDNLPLFMDPLKLLKLTIG 57  
DB 166 MGILLIILISILSFAVATILNNIVNIKKLVYATSIANNLALADIHINSSDELG 245

QY 58 I---SVEHLVEGLKCVNELGPEAS-----EAVKLLLEALS 90  
DB 246 VLAESFNKVRMLRSLINKINTESSNVTDAAYNLQNTQSSKALEQIA 294

RESULT 8  
T05268  
Hypothetical protein T4L20.60 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 26-Aug-1999  
C:Accession: T05268  
R:Bevan, M.; Terry, N.; Ardiles, W.; Buyssehaert, C.; Dasseville, R.; De Clerck, R.; De  
ewes, H.W.; Mayer, K.F.X.; Schueller, C.  
submitted to the Protein Sequence Database, September 1998  
A:Reference number: Z15406  
A:Accession: T05268  
A:Molecule type: DNA  
A:Residues: 1-335 <BEV>  
A:Cross-references: EMBL:AL023094  
A:Experimental source: cultivar Columbia; BAC clone T4L20  
C:Genetics:  
A:Map position: 4  
A>Note: intron positions not resolved  
A:Note: T4L20.60  
C:Superfamily: beta-1,3-glucanase

Query Match 14.9%; Score 68.5; DB 2; Length 335;  
Best Local Similarity 40.0%; Pred. No. 20;  
Matches 20; Conservative 10; Mismatches 17; Indels 3; Gaps 2;

QY 41 NILPFMDPLKLLKLTIGISVEHLVEGLKCVNELGPEASFAVKLLLEALS 90  
DB 80 NVLPFFYPASKIMLTITVGNEI--LMSNDPNLVNQLLP-AMQNVQKALEAVS 126

RESULT 9  
D85406  
Hypothetical protein ATg934480 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 02-Mar-2001  
C:Accession: D85406  
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488; PMID:10617198  
A:Accession: D85406  
A>Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-356 <STO>  
A:Cross-references: GB:NC\_001268; NID:g7270398; PIDN:CAB80165.1; GSPDB:GN00140  
C:Genetics:  
A:Gene: ATg934480  
A:Map position: 4  
C:Superfamily: beta-1,3-glucanase

Query Match 14.9%; Score 68.5; DB 2; Length 356;  
Best Local Similarity 40.0%; Pred. No. 21;  
Matches 20; Conservative 10; Mismatches 17; Indels 3; Gaps 2;

QY 41 NILPFMDPLKLLKLTIGISVEHLVEGLKCVNELGPEASFAVKLLLEALS 90  
DB 101 NVLPFFYPASKIMLTITVGNEI--LMSNDPNLVNQLLP-AMQNVQKALEAVS 147

RESULT 10  
T47710  
Glucuronosyl transferase-like protein - Arabidopsis thaliana  
N:Alternate names: protein F1116.120  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 19-May-2000  
C:Accession: T47710  
R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer,  
submitted to the Protein Sequence Database, March 2000  
A:Reference number: Z24473  
A:Accession: T47710  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-454 <BEN>  
A:Cross-references: EMBL:AL161667  
A:Experimental source: cultivar Columbia; BAC clone F1116  
C:Genetics:  
A:Map position: 3  
A:Introns: 162/1  
A:Note: F1116.120  
C:Superfamily: flavonol O3-glucosyltransferase

Query Match 14.9%; Score 68.5; DB 2; Length 464;  
Best Local Similarity 30.6%; Pred. No. 28;  
Matches 22; Conservative 15; Mismatches 28; Indels 7; Gaps 3;

QY 13 SLCSYSATAPFLINKVPLVDKLAPLPDNLPLFMDPLKLLKLTIGISVEHLVEGLKCVN 72  
DB 142 TFCAYTAPFLIDKGVLPQSSR---LDELVTLPFLK--VKDLPVKTKEPGLNRIIN 196

QY 73 EL--GPEASEAV 82  
DB 197 DMVEGAKLSSGV 208

RESULT 11  
WMVZAI  
A-type inclusion protein - cowpox virus (strain CPRO6)  
C:Species: cowpox virus  
C>Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 16-Jun-2000  
C:Accession: JQ0006; S01495  
R:Funahashi, S.; Sato, T.; Shida, H.  
J. Gen. Virol. 69, 35-47, 1988  
A:Title: Cloning and characterization of the gene encoding the major protein of the  
A:Reference number: JQ0006; MUID:88089536; PMID:2826668  
A:Accession: JQ0006  
A:Molecule type: DNA  
A:Residues: 1-1284 <FUN>  
A:Cross-references: GB:D00319; NID:g221140; PIDN:BAA00222.1; PID:g221141  
R:Patel, D.D.; Pickup, D.J.  
EMBO J. 6, 3787-3794, 1987  
A:Title: Messenger RNAs of a strongly-expressed late gene of cowpox virus contain 5'  
A:Reference number: S01494; MUID:8811568; PMID:2828037  
A:Accession: S01495  
A:Molecule type: DNA  
A:Residues: 1-109 <PAT>

A;Cross-references: EMBL:X06343  
C;Superfamily: cowpox virus A-type inclusion protein  
C;Keywords: inclusion protein

Query Match 14.9%; Score 68.5; DB 1; Length 1284;  
Best Local Similarity 36.0%; Pred. No. 82;  
Matches 27; Conservative 7; Mismatches 24; Indels 17; Gaps 5;  
QY 30 PVDKGLAPLDNL---PWDP--LKLLKT-LGIS-----VEHLVEGLRKCQNELG--- 75  
Db 364 PVKVGSKDDGITYNPEDPDYPTITKTLGIADYQLVINKLIEWLDKCEEGNGG 423  
QY 76 ---PEASEAVKKLE 87  
Db 424 EYKTELEAKRKLE 438

RESULT 12  
RPPFF5  
immunity repressor protein - Bacillus phage phi-105  
C;Species: Bacillus subtilis  
A;Note: host Bacillus subtilis  
C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 16-Jun-2000  
C;Accession: A93579; A91535; S02459; T13543; A24339; A24521  
R;Dhaese, P.; Seurinck, J.; De Smet, B.; Van Montagu, M.  
Nucleic Acids Res. 13, 5441-5455, 1985  
A;Title: Nucleotide sequence and mutational analysis of an immunity repressor gene from  
A;Reference number: A93579; MUID:85297750; PMID:2993999  
A;Accession: A93579  
A;Molecule type: DNA  
A;Residues: 1-147 <DHA>  
A;Cross-references: GB:X02799; NID:g15455; PIDN:CAA26567.1; PID:g579178  
R;Cully, D.F.; Garro, A.J.  
Gene 38, 153-164, 1985

A;Title: Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophage phi-105  
A;Reference number: A91535; MUID:86056972; PMID:3934047  
A;Accession: A91535  
A;Molecule type: DNA  
A;Residues: 1-147 <CUL>  
R;van Kaer, L.; Gansseman, Y.; van Montagu, M.; Dhaese, P.  
EMBO J. 7, 859-866, 1988  
A;Title: Interaction of the Bacillus subtilis phage phi105 repressor with operator DNA:  
A;Reference number: S02459; MUID:88283656; PMID:3135184  
A;Accession: S02459  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 4-147 <VAN>  
A;Note: part of this sequence, including the amino end of the mature protein, was confirmed by R;Kobayashi, K.; Okamura, K.; Inoue, T.; Sato, T.; Kobayashi, Y.  
submitted to the EMBL Data Library, July 1998  
A;Description: Complete nucleotide sequence of Bacillus subtilis phage phi-105.  
A;Reference number: 217688  
A;Accession: T13543  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 4-147 <KOB>  
A;Cross-references: EMBL:AB016282; PIDN:BAA36660.1  
C;Genetics:  
A;Start codon: GTG  
C;Superfamily: phage phi-105 immunity repressor protein  
C;Keywords: DNA binding; early protein; repressor; transcription regulation

Query Match 14.8%; Score 68; DB 1; Length 147;  
Best Local Similarity 24.3%; Pred. No. 9.2;  
Matches 25; Conservative 13; Mismatches 33; Indels 32; Gaps 2;  
QY 23 LINKVPLPVDKLAFLPDLNLPFMDPLKLLKTGLISVEHLV----- 64  
Db 24 LAEKANLSRSLADIERDYNPSLSTLEAVAGALQVSAIVGEETLKEEQAEYNKEE 83  
QY 65 -----EGLRKCQNELG-----PEASEAVKKLEALSHLV 93  
Db 84 KDIAKMEIEIRKDLKSDGLSFGSPMSQEAIVESLMEAHIV 126

RESULT 13  
D70359  
conserved hypothetical protein aq\_674 - Aquifex aeolicus  
C;Species: Aquifex aeolicus  
C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 05-Nov-1999  
C;Accession: D70359  
R;Decker, G.; Warren, P.V.; Gaaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.  
V.  
Nature 392, 353-358, 1998  
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A;Reference number: A70300; MUID:98196666; PMID:9537320  
A;Accession: D70359  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-239 <AQF>  
A;Cross-references: GB:AE000701; NID:g2983260; PIDN:AAC06868.1; PID:g2983274; GB:AE01  
A;Experimental source: strain VF5  
C;Genetics:  
A;Gene: aq\_674

Query Match 14.8%; Score 68; DB 2; Length 239;  
Best Local Similarity 32.6%; Pred. No. 15;  
Matches 28; Conservative 15; Mismatches 27; Indels 16; Gaps 5;  
QY 9 LVTISLC--SYSATAPLINKVPLPVDKLAFLPDLNLPFMDPLKLLKTGLISVEHLV 66  
Db 160 LVLLSPCFRLYELTEVLSN-FNLPRLKLS-----LIYPTLKRARLAITVSVKN-VKG 210  
QY 67 LRKC-----VNELGPEASEAVKKLE 87  
Db 211 QLECDKPLIINKENGEYTBVKQLLE 236

RESULT 14  
C86364  
hypothetical protein F19G10.4 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 19-Apr-2002  
C;Accession: C86364  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Ali  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.B.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: C86364  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-693 <STO>  
A;Cross-references: GB:AE005172; NID:g2462833; PIDN:AAB72168.1; GSPDB:GN00141  
C;Genetics:  
A;Map position: 1  
C;Superfamily: ferric reductase FRE2

Query Match 14.8%; Score 68; DB 2; Length 693;  
Best Local Similarity 31.8%; Pred. No. 48;  
Matches 34; Conservative 14; Mismatches 37; Indels 22; Gaps 5;  
QY 6 IFLL-VTISLCSYSATAPLINK-----VPLPVDKLAFLP-----DNILPFMDPL----- 49  
Db 584 IYLLAISVIGVATSTVAMLCNKKSYFKGLYQNVDAISPLMIESPDQLLEFNTIHYGER 643  
QY 50 ----KLLKLTGLISVEHLVEGLRKCQNELGPEAS--EAVKKLEALS 90  
Db 644 PNLKLLVGLKSSVGVIVCGPRKREEVAKICFSGSAANLQFESIS 690

Search completed: June 2, 2004, 20:22:20  
Job time : 8.33063 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:19:10 ; Search time 16.5802 Seconds  
(without alignments)  
1578.054 Million cell updates/sec

Title: US-09-700-770-7

Perfect score: 459

Sequence: 1 MKLVTFILVILSLCSYSAT.....LGPEASEAVKKLLRLSLHLV 93

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/prodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	459	100.0	93	12	US-10-206-915-244
2	459	100.0	93	12	US-10-199-670-244
3	459	100.0	93	12	US-10-201-858-244
4	459	100.0	93	12	US-10-205-890-244
5	459	100.0	93	12	US-10-208-024-244
6	459	100.0	93	12	US-10-201-853-244
7	459	100.0	93	12	US-10-174-581-244
8	459	100.0	93	12	US-10-176-483-244
9	459	100.0	93	12	US-10-176-749-244
10	459	100.0	93	12	US-10-176-914-244
11	459	100.0	93	12	US-10-176-915-244
12	459	100.0	93	12	US-10-176-484-244
13	459	100.0	93	12	US-10-180-550-244
14	459	100.0	93	12	US-10-183-014-244
15	459	100.0	93	12	US-10-187-738-244

16	459	100.0	93	12	US-10-187-740-244
17	459	100.0	93	12	US-10-187-883-244
18	459	100.0	93	12	US-10-194-363-244
19	459	100.0	93	12	US-10-194-460-244
20	459	100.0	93	12	US-10-194-463-244
21	459	100.0	93	12	US-10-194-484-244
22	459	100.0	93	12	US-10-195-884-244
23	459	100.0	93	12	US-10-195-896-244
24	459	100.0	93	12	US-10-196-744-244
25	459	100.0	93	12	US-10-196-755-244
26	459	100.0	93	12	US-10-196-757-244
27	459	100.0	93	12	US-10-197-704-244
28	459	100.0	93	12	US-10-197-710-244
29	459	100.0	93	12	US-10-198-758-244
30	459	100.0	93	12	US-10-198-766-244
31	459	100.0	93	12	US-10-199-304-244
32	459	100.0	93	12	US-10-199-309-244
33	459	100.0	93	12	US-10-199-313-244
34	459	100.0	93	12	US-10-199-456-244
35	459	100.0	93	12	US-10-201-329-244
36	459	100.0	93	12	US-10-202-412-244
37	459	100.0	93	12	US-10-206-919-244
38	459	100.0	93	12	US-10-206-922-244
39	459	100.0	93	12	US-10-206-924-244
40	459	100.0	93	12	US-10-206-928-244
41	459	100.0	93	12	US-10-207-914-244
42	459	100.0	93	12	US-10-207-921-244
43	459	100.0	93	12	US-10-207-922-244
44	459	100.0	93	12	US-10-208-027-244
45	459	100.0	93	12	US-10-174-570-244

## ALIGNMENTS

### RESULT 1

US-10-206-915-244  
; Sequence 244, Application US/10206915  
; Publication No. US20040029221A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P34301C513  
; CURRENT APPLICATION NUMBER: US/10/206,915  
; CURRENT FILING DATE: 2002-07-26  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541

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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-206-915-244

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Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFILVTISLCSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTIGISV 60
DB 1 MKLVTFILVTISLCSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTIGISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93
DB 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93

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RESULT 2
US-10-199-670-244
; Sequence 244, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C401
; CURRENT APPLICATION NUMBER: US/10/199,670
; CURRENT FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-670-244

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Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFILVTISLCSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTIGISV 60
DB 1 MKLVTFILVTISLCSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTIGISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93
DB 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93

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RESULT 3
US-10-201-858-244
; Sequence 244, Application US/10201858
; Publication No. US2004003837A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-858-244

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```

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLVTFILVTISLCSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTIGISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93
DB 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93

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RESULT 4
US-10-205-890-244
; Sequence 244, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-890-244

Query Match          100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKLVTFLLVTLSCSYSAFLINKVPLPVDKLAFLPLDNLFPFMDPLKLLKLTIGISV 60

QY 61 EHLVEGLRKCVELGPEASEAVKLEALSHLV 93
Db 61 EHLVEGLRKCVELGPEASEAVKLEALSHLV 93

RESULT 5
US-10-208-024-244
; Sequence 244, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
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```
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C538
; CURRENT APPLICATION NUMBER: US/10/208,024
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-208-024-244
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Query Match          100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTLSCSYSAFLINKVPLPVDKLAFLPLDNLFPFMDPLKLLKLTIGISV 60
Db 1 MKLVTFLLVTLSCSYSAFLINKVPLPVDKLAFLPLDNLFPFMDPLKLLKLTIGISV 60

QY 61 EHLVEGLRKCVELGPEASEAVKLEALSHLV 93
Db 61 EHLVEGLRKCVELGPEASEAVKLEALSHLV 93
```

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RESULT 6
US-10-201-853-244
; Sequence 244, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
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Query Match          100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTLSCSYSAFLINKVPLPVDKLAFLPLDNLFPFMDPLKLLKLTIGISV 60
Db 1 MKLVTFLLVTLSCSYSAFLINKVPLPVDKLAFLPLDNLFPFMDPLKLLKLTIGISV 60

QY 61 EHLVEGLRKCVELGPEASEAVKLEALSHLV 93
Db 61 EHLVEGLRKCVELGPEASEAVKLEALSHLV 93

RESULT 6
US-10-201-853-244
; Sequence 244, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
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; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
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; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
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; PRIOR APPLICATION NUMBER: 60/078939
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; PRIOR FILING DATE: 1998-03-27
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1997-10-24

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFILVTSLSYSATAFINKVPLVDKLAFLPDNLTLPFMDPKLLKLTGISV 60
Db 1 MKLVTFILVTSLSYSATAFINKVPLVDKLAFLPDNLTLPFMDPKLLKLTGISV 60

QY 61 EHLVEGLRKCVELGPEASEAVKKLEALSHLV 93
Db 61 EHLVEGLRKCVELGPEASEAVKKLEALSHLV 93

RESULT 7
US-10-174-581-244
; Sequence 244, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
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; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
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; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1997-10-24

; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-201-853-244
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Db 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
QY 61 EHLVEGLRKCYNELGPEASEAVKLLLEALSHLV 93
Db 61 EHLVEGLRKCYNELGPEASEAVKLLLEALSHLV 93

RESULT 9
US-10-176-749-244
; Sequence 244, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176, 749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-244

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
Db 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60

RESULT 10
US-10-176-914-244
; Sequence 244, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176, 914
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-914-244

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
Db 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60

RESULT 11
US-10-176-915-244
; Sequence 244, Application US/10176915
; Publication No. US20030017544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C110
; CURRENT APPLICATION NUMBER: US/10/176, 915
; CURRENT FILING DATE: 2002-06-21
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-915-244

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
Db 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60

RESULT 12
US-10-176-484-244
; Sequence 244, Application US/10176484
; Publication No. US20030059876A9
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
```

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; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-914-244

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
Db 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60

RESULT 9
US-10-176-749-244
; Sequence 244, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176, 749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-244

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
Db 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60

RESULT 10
US-10-176-914-244
; Sequence 244, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176, 914
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-914-244

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
Db 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60

RESULT 11
US-10-176-915-244
; Sequence 244, Application US/10176915
; Publication No. US20030017544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C110
; CURRENT APPLICATION NUMBER: US/10/176, 915
; CURRENT FILING DATE: 2002-06-21
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-915-244

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
Db 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60

RESULT 12
US-10-176-484-244
; Sequence 244, Application US/10176484
; Publication No. US20030059876A9
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
```

```

; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C64
; CURRENT APPLICATION NUMBER: US/10/176,484
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-176-484-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSICSYSAFAFLINKVPLPVDKLAFLPLDNLPLPMDPLKLLKLTGLISV 60
Db 1 MKLVTFLLVTSICSYSAFAFLINKVPLPVDKLAFLPLDNLPLPMDPLKLLKLTGLISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93
Db 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93

RESULT 13
US-10-180-550-244
; Sequence 244, Application US/10180550
; Publication No. US20030064440A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C149
; CURRENT APPLICATION NUMBER: US/10/180,550
; CURRENT FILING DATE: 2002-06-25
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-180-550-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSICSYSAFAFLINKVPLPVDKLAFLPLDNLPLPMDPLKLLKLTGLISV 60
Db 1 MKLVTFLLVTSICSYSAFAFLINKVPLPVDKLAFLPLDNLPLPMDPLKLLKLTGLISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93
Db 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93

RESULT 14
US-10-180-550-244
; Sequence 244, Application US/10180550
; Publication No. US20030064440A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C149
; CURRENT APPLICATION NUMBER: US/10/180,550
; CURRENT FILING DATE: 2002-06-25
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-180-550-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSICSYSAFAFLINKVPLPVDKLAFLPLDNLPLPMDPLKLLKLTGLISV 60
Db 1 MKLVTFLLVTSICSYSAFAFLINKVPLPVDKLAFLPLDNLPLPMDPLKLLKLTGLISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93
Db 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93

RESULT 15
US-10-187-738-244
; Sequence 244, Application US/10187738
; Publication No. US20030064442A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C241
; CURRENT APPLICATION NUMBER: US/10/187,738
; CURRENT FILING DATE: 2003-07-02
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-187-738-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-10-183-014-244
; Sequence 244, Application US/10183014
; Publication No. US20030064441A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C170
; CURRENT APPLICATION NUMBER: US/10/183,014
; CURRENT FILING DATE: 2002-06-26
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-183-014-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSICSYSAFAFLINKVPLPVDKLAFLPLDNLPLPMDPLKLLKLTGLISV 60
Db 1 MKLVTFLLVTSICSYSAFAFLINKVPLPVDKLAFLPLDNLPLPMDPLKLLKLTGLISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93
Db 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93

RESULT 16
US-10-187-738-244
; Sequence 244, Application US/10187738
; Publication No. US20030064442A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C241
; CURRENT APPLICATION NUMBER: US/10/187,738
; CURRENT FILING DATE: 2003-07-02
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-187-738-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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us-09-700-770-7.rapb

Thu Jun 3 10:25:03 2004

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Db	1		60
Qy	61	EHLVEGLRKCYNELGPEASEAVKKLEALSHLV	93
Db	61		93

Search completed: June 2, 2004, 20:25:18  
Job time : 17.5802 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 20:16:40 ; Search time 6.48136 Seconds  
(without alignments)  
740.773 Million cell updates/sec

Title: US-09-700-770-7  
Perfect score: 459  
Sequence: 1 MKLVITFLVLTISLCSYSAT.....LGPEASEAVKLLLEALSHLV 93

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	459	100.0	93	2	US-08-964-725-14
2	84	18.3	17	2	US-08-964-725-15
3	77	16.8	15	2	US-08-964-725-18
4	77	16.8	18	2	US-08-964-725-19
5	76	16.6	17	2	US-08-964-725-17
6	75.5	16.4	90	3	US-08-821-451A-4
7	75.5	16.4	90	3	US-09-263-810-4
8	75.5	16.4	90	3	US-08-912-276-15
9	75.5	16.4	90	4	US-09-583-169-4
10	75.5	16.4	90	4	US-09-215-818-6
11	75.5	16.4	90	4	US-09-467-602A-6
12	73	15.9	446	4	US-09-134-000C-3434
13	69	15.0	95	3	US-08-821-451A-27
14	69	15.0	95	3	US-09-263-810-27
15	69	15.0	95	4	US-09-583-169-27
16	67.5	14.7	421	4	US-09-328-352-7140
17	67	14.6	95	1	US-08-455-896-7
18	67	14.6	95	2	US-08-933-149-7
19	67	14.6	95	2	US-09-082-343-7
20	67	14.6	95	3	US-09-082-253-7
21	67	14.6	95	4	US-09-162-622-7
22	67	14.6	95	4	US-09-509-015-7
23	67	14.6	95	5	PCT-US96-08235-7
24	66.5	14.5	91	1	US-08-455-896-8
25	66.5	14.5	91	2	US-08-933-149-8
26	66.5	14.5	91	2	US-09-082-343-8
27	66.5	14.5	91	3	US-09-082-253-8

Sequence 1, Appli  
Sequence 8, Appli  
Sequence 8, Appli  
Sequence 8, Appli  
Sequence 2, Appli  
Sequence 5830, Ap  
Sequence 28767, A  
Sequence 4739, Ap  
Sequence 16, Appli  
Sequence 6, Appli  
Sequence 6372, Ap  
Sequence 9300, Ap  
Sequence 22, Appli  
Sequence 22, Appli  
Sequence 3880, Ap  
Sequence 21, Appli  
Sequence 7, Appli  
Sequence 7, Appli

## ALIGNMENTS

RESULT 1  
US-08-964-725-14  
; Sequence 14, Application US/08964725  
; Patent No. 5939265  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, Maurice  
; APPLICANT: FRIEDMAN, Paula N.  
; APPLICANT: GORDON, Julian  
; APPLICANT: HODGES, Steven C.  
; APPLICANT: KLASS, Michael R.  
; APPLICANT: KRATOCHVIL, Jon D.  
; APPLICANT: ROBERTS-RAPP, Lisa  
; APPLICANT: RUSSELL, John C.  
; APPLICANT: STROUPE, Steven D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/964,725  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 5997.US.PI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 93 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

MOLECULE TYPE: No. 5939265e  
US-08-964-725-14

Query Match 100.0%; Score 459; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 2.8e-47;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLVTFILVITSLCSYATATFLINKVPLVDKLAFLPMDPKLLKLTGTSV 60  
Db 1 MKLVTFILVITSLCSYATATFLINKVPLVDKLAFLPMDPKLLKLTGTSV 60

Qy 61 EHLVEGLRKCVELGPEASEAVKLEALSHLV 93  
Db 61 EHLVEGLRKCVELGPEASEAVKLEALSHLV 93

RESULT 2  
US-08-964-725-15  
Sequence 15, Application US/08964725  
Patent No. 5939265

GENERAL INFORMATION:  
APPLICANT: COHEN, Maurice  
APPLICANT: FRIEDMAN, Paula N.  
APPLICANT: GORDON, Julian  
APPLICANT: HODGES, Steven C.  
APPLICANT: KLAS, Michael R.  
APPLICANT: KRATOCHVIL, Jon D.  
APPLICANT: ROBERTS-RAPP, Lisa  
APPLICANT: RUSSELL, John C.  
APPLICANT: STROUPE, Steven D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE LUNG  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,725  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 5997.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5939265e  
US-08-964-725-15

Query Match 18.3%; Score 84; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 NKVLPVVDKLAFLPLD 40  
Db 1 NKVLPVVDKLAFLPLD 16

RESULT 3  
US-08-964-725-18  
Sequence 18, Application US/08964725  
Patent No. 5939265

GENERAL INFORMATION:  
APPLICANT: COHEN, Maurice  
APPLICANT: FRIEDMAN, Paula N.  
APPLICANT: GORDON, Julian  
APPLICANT: HODGES, Steven C.  
APPLICANT: KLAS, Michael R.  
APPLICANT: KRATOCHVIL, Jon D.  
APPLICANT: ROBERTS-RAPP, Lisa  
APPLICANT: RUSSELL, John C.  
APPLICANT: STROUPE, Steven D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE LUNG  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,725  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 5997.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5939265e  
US-08-964-725-18

Query Match 16.8%; Score 77; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0072;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 LRKCVNELGPEASEA 81  
Db 1 LRKCVNELGPEASEA 15

RESULT 4  
US-08-954-725-19  
Sequence 19, Application US/08964725  
Patent No. 5939265  
GENERAL INFORMATION:  
APPLICANT: COHEN, Maurice

```

; APPLICANT: FRIEDMAN, Paula N.
; APPLICANT: GORDON, Julian C.
; APPLICANT: HODGES, Steven C.
; APPLICANT: KLASS, Michael R.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: ROBERTS-RAPP, Lisa
; APPLICANT: RUSSELL, John C.
; APPLICANT: STROUPE, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,725
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5997.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5939265e
; US-08-964-725-19

Query Match 16.8%; Score 77; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 EASEAVKKLLEALSHLV 93
Db 1 EASEAVKKLLEALSHLV 17

RESULT 5
US-08-964-725-17
; Sequence 17, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
; APPLICANT: FRIEDMAN, Paula N.
; APPLICANT: GORDON, Julian
; APPLICANT: HODGES, Steven C.
; APPLICANT: KLASS, Michael R.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: ROBERTS-RAPP, Lisa
; APPLICANT: RUSSELL, John C.
; APPLICANT: STROUPE, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 19

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,725
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5997.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5939265e
; US-08-964-725-17

Query Match 16.6%; Score 76; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 LKLTGLGIVHVLVEGL 67
Db 1 LKLTGLGIVHVLVEGL 16

RESULT 6
US-08-821-451A-4
; Sequence 4, Application US/08821451A
; Patent No. 6066724
; GENERAL INFORMATION:
; APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
; TITLE OF INVENTION: Human Endometrial Specific Steroid-
; TITLE OF INVENTION: Binding Factor I, II and III
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821,451A
; FILING DATE: March 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/014,724

```



```

; FILING DATE: March 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-821-451A-4

Query Match 16.4%; Score 75.5; DB 3; Length 90;
Best Local Similarity 27.0%; Pred. No. 0.11;
Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;

QY 1 MKLVTFLLVTVISLCSYSATFLINKVPLPVDKLAFLPLDNLPLFM--DPL-KLLKTL 56
Db 1 MKLSVCLLVTLALCCYQANA-----EFCPALVSELLDFFIFSEPLFKLSAKF 49
QY 57 GISVEHLVE--GLRKCVNELGPE----ASEAVKKILEALS 90
Db 50 DAPEAAVAKLGIVKRCCTDQMSLQKRSLIAEVLVKLKCS 89

RESULT 7
US-09-263-810-4
; Sequence 4, Application US/09263810
; Patent No. 6174992
; GENERAL INFORMATION:
; APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
; TITLE OF INVENTION: Human Endometrial Specific Steroid-
; TITLE OF INVENTION: Binding Factor I, II and III
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAPELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,810
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/821,451
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN

```





Thu Jun 3 10:25:03 2004

Matches 25; Conservative 21; Mismatches 37; Indels 8; Gaps 3;  
Qy 1 MKLVTFLLVTVISCSY-SATAFLINKVPLVDKLAFLDNLPLFMDPLKLLKLTGIS 59  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 1 MKLVFLFLLVTVIPICCVASGCSI-----LDEVIRGTINSTVTLHDYMKLVKPYVQAH 54  
Qy 60 -VEHLVEGLRKCVELGPEASEAVKLLLEAL 89  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 55 FTEKAVKQKQCFDQTDKLTLENVGVNMEAI 85

RESULT 15

US-09-583-169-27  
; Sequence 27, Application US/09583169  
; Patent No. 6338948  
; GENERAL INFORMATION:  
; APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
; TITLE OF INVENTION: Human Endometrial Specific Steroid-  
; TITLE OF INVENTION: Binding Factor I, II and III  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESS: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/583,169  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/821,451  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 95 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
US-09-583-169-27

Query Match 15.0%; Score 69; DB 4; Length 95;  
Best Local Similarity 27.5%; Pred.No. 0.71; 37; Indels 8; Gaps 3;  
Matches 25; Conservative 21; Mismatches 37; Indels 8; Gaps 3;  
Qy 1 MKLVTFLLVTVISCSY-SATAFLINKVPLVDKLAFLDNLPLFMDPLKLLKLTGIS 59  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 1 MKLVFLFLLVTVIPICCVASGCSI-----LDEVIRGTINSTVTLHDYMKLVKPYVQAH 54  
Qy 60 -VEHLVEGLRKCVELGPEASEAVKLLLEAL 89  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 55 FTEKAVKQKQCFDQTDKLTLENVGVNMEAI 85

Search completed: June 2, 2004, 20:23:15  
Job time : 7.48136 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2004, 19:59:24 ; Search time 22.1572 Seconds  
(without alignments)  
1185.931 Million cell updates/sec

Title: US-09-700-770-7  
Perfect score: 459  
Sequence: 1 MKLVITFLVTLISLCSYAT.....LGPSEAVKLLLEALSHLV 93

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	459	100.0	93	2 AAW62068	Aaw62068 Human lun
2	459	100.0	93	2 AAY28334	Aay28334 LU103 spe
3	459	100.0	93	3 AAY44456	Aay44456 Human lun
4	459	100.0	93	3 AAY87289	Aay87289 Human sig
5	459	100.0	93	4 AAU29145	Aau29145 Human PRO
6	459	100.0	93	6 ABUS5821	Abu58521 Human PRO
7	459	100.0	93	6 ABUS8069	Abu8069 Novel hum
8	459	100.0	93	6 ABUS84384	Abu84384 Human sec
9	459	100.0	93	6 ABR66258	Abu66258 Human sec
10	459	100.0	93	6 ABR65648	Abu65648 Human sec
11	459	100.0	93	6 ABUS9588	Abu9588 Human sec
12	459	100.0	93	6 ABUS92827	Abu82827 Human PRO
13	459	100.0	93	6 ABUS9948	Abu9948 Novel hum
14	459	100.0	93	6 ABR68197	Abu68197 Human sec
15	459	100.0	93	6 AAO19894	Aao19894 Human ute
16	459	100.0	93	6 ABUS96250	Abu96250 Novel hum
17	459	100.0	93	6 ABUS92681	Abu92681 Human sec
18	459	100.0	93	6 ABO08758	Abo08758 Human sec
19	459	100.0	93	6 ABO02810	Abo02810 Human sec
20	459	100.0	93	6 ABR74964	Abu74964 Human sec
21	459	100.0	93	6 ABR94726	Abu94726 Human sec
22	459	100.0	93	6 ABUS5699	Abu5699 Human PRO
23	459	100.0	93	6 ABUS9859	Abu9859 Novel hum
24	459	100.0	93	6 ABUS98074	Abu98074 Novel hum
25	459	100.0	93	6 ABUS91780	Abu91780 Novel hum

ALIGNMENTS

RESULT 1

AAW62068  
ID AAW62068 standard; protein; 93 AA.  
XX  
AC AAW62068;  
XX  
DT 14-SEP-1998 (first entry)  
XX  
DE Human lung tissue gene LU103 protein.  
XX  
KW Human; lung tissue gene; LU103; detection; lung cancer; diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN W09H20143-A1.  
XX  
PD 14-MAY-1998.  
XX  
PF 05-NOV-1997; 97WO-US020680.  
XX  
PR 05-NOV-1996; 96US-00744211.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Cohen M, Friedman PN, Gordon J, Hodges SC, Klass MR;  
PI Kratochwill JD, Roberts-Rapp L, Russell JC, Stroupe SD;  
XX  
DR WPI: 1998-286957/25.  
XX  
N-PSDB; AAV38069, AAV38070.  
XX  
PT Lung tissue derived polynucleotide LU103 - useful to detect, diagnose, stage, monitor, prognosis, prevent, treat or determine pre-disposition to lung disease, e.g. lung cancer.  
XX  
PS Claim 20; Page 70; 86pp; English.

The present sequence represents the protein for lung tissue gene LU103. A method has been developed for detecting the presence of a target LU103 polynucleotide in a test sample, comprising: (a) contacting the sample with at least 1 LU103-specific polynucleotide, and (b) detecting the target LU103 polynucleotide in the test sample, where the LU103 polynucleotide has at least 50% identity to the 269, 263, 225, 507 or 519 bp nucleic acid sequence given in AAV38066 to AAV38070. The methods and products of the present invention may be used to detect, diagnose, stage, monitor, prognosis, prevent, treat or determine the predisposition diseases and conditions of the lung, e.g. lung cancer  
Sequence 93 AA;

Abu89473 Human PRO  
Abu86314 Human sec  
Abu67527 Human sec  
Abu80555 Human PRO  
Abu99473 Human sec  
Abu98863 Human sec  
Abu16386 Human sec  
Abu92286 Human sec  
Abu18927 Human sec  
Abu78348 Human sec  
Abu85084 Novel hum  
Abu00223 Novel hum  
Abu11555 Human sec  
Abu02200 Human sec  
Abu8774 Novel hum  
Abu83469 Human sec  
Abu06270 Novel hum  
Abu59306 Human sec  
Abu0368 Human sec  
Abu19232 Novel hum

459 100.0 93 6 ABUS9473  
459 100.0 93 6 ABUS6314  
459 100.0 93 6 ABUS7527  
459 100.0 93 6 ABUS0555  
459 100.0 93 6 ABUS9473  
459 100.0 93 6 ABUS8863  
459 100.0 93 6 ABUS16386  
459 100.0 93 6 ABUS92286  
459 100.0 93 6 ABUS18927  
459 100.0 93 6 ABUS78348  
459 100.0 93 6 ABUS5084  
459 100.0 93 6 ABUS00223  
459 100.0 93 6 ABUS11555  
459 100.0 93 6 ABUS02200  
459 100.0 93 6 ABUS8774  
459 100.0 93 6 ABUS83469  
459 100.0 93 6 ABUS06270  
459 100.0 93 6 ABUS59306  
459 100.0 93 6 ABUS0368  
459 100.0 93 6 ABUS19232

Thu Jun 3 10:25:02 2004

us-09-700-770-7.rag

Db 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93

Query Match 100.0%; Score 459; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-47;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPLDNLTPMDPLKLLKLTGLISV 60  
 Db 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPLDNLTPMDPLKLLKLTGLISV 60  
 QY 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93  
 Db 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93

RESULT 2  
 AAY28334  
 ID AAY28334 standard; protein; 93 AA.

XX AC AAY28334;  
 XX 19-OCT-1999 (first entry)  
 XX LU103 specific amino acid consensus sequence.  
 DE LU103; amino acid; lung cancer; detection; FISH;  
 KW Fluorescent in situ hybridisation; protein.  
 XX Synthetic.  
 OS Homo sapiens.  
 OS US5939265-A.  
 XX 17-AUG-1999.  
 XX 05-NOV-1997; 97US-00964725.  
 XX 05-NOV-1996; 96US-00744211.  
 PR XX (ABBO ) ABBOTT LAB.  
 XX Friedman PN, Gordon J, Hodges SC, Cohen M, Kratochvil JD;  
 PI Roberts-Rapp L, Russell JC, Stroupe SD, Klass MR;  
 XX WPI; 1998-468402/39.  
 DR N-PSDB; AAX99424.

Polynucleotides useful for detecting, diagnosing and monitoring diseases of the lung such as lung cancer.  
 XX Claim 20; Col 53; 36pp; English.  
 XX The 507 base pair sequence of a LU103 specific polynucleotide was derived from a consensus of the isolated sequences from clones 1235095, 1235531 and 1379417. This sequence was then scanned for open reading frames. An ORF was found and this polypeptide was produced. The polynucleotides and methods are useful for detecting, diagnosing, staging, monitoring or predicting diseases and conditions of the lung, such as lung cancer. The polynucleotides may be used to produce probes for use in fluorescent in situ hybridization (FISH) technology to perform chromosomal analysis and identify cancer specific alterations such as deletions

XX SQ Sequence 93 AA;  
 Query Match 100.0%; Score 459; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-47;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPLDNLTPMDPLKLLKLTGLISV 60  
 Db 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPLDNLTPMDPLKLLKLTGLISV 60  
 QY 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93

Db 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93  
 RESULT 3  
 AAY44456  
 ID AAY44456 standard; protein; 93 AA.  
 XX AC AAY44456;  
 XX 27-MAR-2000 (first entry)  
 DT Human lung specific gene protein Lng101.  
 DE Lung Specific Gene; LSG; Lng101; human; diagnostic marker; prognosticate;  
 KW lung cancer; diagnosis.  
 XX Homo sapiens.  
 OS WO9960160-A1.  
 XX 25-NOV-1999.  
 PD 12-MAY-1999; 99WO-US010344.  
 PF 21-MAY-1998; 98US-0086212P.  
 PR (DIAD-) DIADEXUS LLC.  
 XX Yang F, Macina RA, Sun Y;  
 PI WPI; 2000-116320/10.  
 DR N-PSDB; AAZ29721.  
 XX A new method for diagnosing, monitoring and staging lung cancer.  
 XX Example 2; Page 36; 40pp; English.  
 XX The present sequence is a lung specific gene (LSG) protein Lng101 from human clone ID 126758. The LSG has high level of tissue specificity for lungs and is overexpressed in cancerous tissues. The sequence serves as a diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnosis involves comparing levels of LSG in samples obtained from patient and normal control  
 XX SQ Sequence 93 AA;  
 Query Match 100.0%; Score 459; DB 3; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-47;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPLDNLTPMDPLKLLKLTGLISV 60  
 Db 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPLDNLTPMDPLKLLKLTGLISV 60  
 QY 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93  
 Db 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93  
 RESULT 4  
 AAY87289  
 ID AAY87289 standard; protein; 93 AA.  
 XX AC AAY87289;  
 XX 11-MAY-2000 (first entry)  
 DT Human signal peptide containing protein HSP66 SEQ ID NO:66.  
 DE Human; signal peptide-containing protein; HSP66; diagnosis; cancer;  
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;  
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;

KW reproductive disorder; developmental disorder; arteriosclerosis;  
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
KW Parkinson's disease; Huntington's disease; ovulatory defect;  
KW muscular dystrophy.  
XX  
OS Homo sapiens.  
XX  
PN WO20000610-A2.  
XX  
XX 06-JAN-2000.  
XX  
XX 25-JUN-1999; 99WO-US014484.  
XX  
XX 26-JUN-1998; 98US-0090762P.  
PR 31-JUL-1998; 98US-0094983P.  
PR 01-OCT-1998; 98US-0102686P.  
PR 11-DEC-1998; 98US-0112129P.  
XX  
XX (INCY-) INCYTE PHARM INC.  
PA  
XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
PI Bandman O;  
XX WPI; 2000-160673/14.  
DR N-PSDB; AAZ98174.  
XX  
XX New human signal peptide-containing proteins useful in treatment,  
PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular  
PT disease.  
XX  
XX Claim 1; Page 206; 327pp; English.  
XX  
XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the  
CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have  
CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,  
CC neuroprotective, cardiovascular and antiasthmatic activities, and can be  
CC used in gene therapy. HSPPs can be used to treat or prevent disorders  
CC associated with decreased activity or function of HSPP. Antagonists of  
CC HSPP are used to treat or prevent disorders associated with increased  
CC activity or function of HSPP. Such diseases include cell proliferation  
CC (including cancer), inflammation, cardiovascular, neurological,  
CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
CC asthma, Crohn's disease, microbial or other infections, congestive or  
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP  
CC nucleic acids can be used for the recombinant production of HSPP, for  
CC detecting HSPP in standard hybridisation and amplification assays (for  
CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming  
CC or ribozyme therapeutics, for detecting related sequences or genetic  
CC variations, and for chromosomal mapping. HSPP are also used to raise  
CC specific antibodies (Ab) and to screen for agonists and antagonists  
CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP  
CC -related diseases (in usual immunoassays), as therapeutic antagonists, in  
CC competitive drug screens, and for purification of HSPP from natural  
CC sources  
XX  
XX Sequence 93 AA;  
SQ  
Query Match 100.0%; Score 459; DB 3; Length 93;  
Best Local Similarity 100.0%; Pred. No. 5.6e-47; Mismatches 0; Gaps 0;  
Matches 93; Conservative 0; Indels 0;  
QY 1 MKLVTFLLVTLISCSYSAFLINKVPLVDVKLAPLDNLIPFMDPLKLLTKTIGISV 60  
Db 1 MKLVTFLLVTLISCSYSAFLINKVPLVDVKLAPLDNLIPFMDPLKLLTKTIGISV 60  
QY 61 EHLVEGLRKCWNLGPEASEAVKKLLEALSHLV 93  
Db 61 EHLVEGLRKCWNLGPEASEAVKKLLEALSHLV 93

RESULT 5  
AAU29145  
ID AAU23145 standard; protein; 93 AA.  
XX  
XX AAU29145;  
XX  
XX 18-DEC-2001 (first entry)  
XX  
XX Human PRO polypeptide sequence #122.  
XX  
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
XX  
XX Homo sapiens.  
XX WO200168848-A2.  
XX  
XX 20-SEP-2001.  
XX  
XX 28-FEB-2001; 2001WO-US006520.  
XX  
XX 01-MAR-2000; 2000WO-US005601.  
XX 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 06-MAR-2000; 2000US-0186968P.  
PR 14-MAR-2000; 2000US-0189320P.  
PR 14-MAR-2000; 2000US-0189328P.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 21-MAR-2000; 2000US-0190828P.  
PR 21-MAR-2000; 2000US-0191007P.  
PR 21-MAR-2000; 2000US-0191048P.  
PR 21-MAR-2000; 2000US-0191314P.  
PR 28-MAR-2000; 2000US-0192655P.  
PR 29-MAR-2000; 2000US-0193032P.  
PR 29-MAR-2000; 2000US-0193053P.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 04-APR-2000; 2000US-0194449P.  
PR 04-APR-2000; 2000US-019647P.  
PR 11-APR-2000; 2000US-0195975P.  
PR 11-APR-2000; 2000US-0196000P.  
PR 11-APR-2000; 2000US-0196187P.  
PR 11-APR-2000; 2000US-0196690P.  
PR 18-APR-2000; 2000US-0198121P.  
PR 18-APR-2000; 2000US-0198585P.  
PR 25-APR-2000; 2000US-0199397P.  
PR 25-APR-2000; 2000US-0199550P.  
PR 25-APR-2000; 2000US-0199654P.  
PR 03-MAY-2000; 2000US-0201516P.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Par J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI; 2001-602746/88.  
DR N-PSDB; AAS46046.  
XX  
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the

Thu Jun 3 10:25:02 2004

us-09-700-770-7.1rag

PT presence of tumors, such as prostate and breast tumors, in mammals and to  
PT screen for modulators of the compounds.

PS Claim 11; Fig 244; 774pp; English.

XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
CC The PRO polypeptides and their associated nucleic acids can be used to  
CC detect the presence of a tumour in a mammal by comparing the level of  
CC expression of a PRO polypeptide in a test sample of cells from the animal  
CC and a control sample of normal cells, whereby a higher level of  
CC expression in the test sample indicates the presence of a tumour in the  
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
CC and rabbits but are preferably human. The polypeptides can be used to  
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
CC when contacted with it. A specific polypeptide can be used to stimulate  
CC the proliferation or differentiation of chondrocyte cells. The PRO  
CC proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders

XX Sequence 93 AA;

Query Match 100.0%; Score 459; DB 4; Length 93;  
Best Local Similarity 100.0%; Pred. No. 5.6e-47;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVLTISLCSYSATAFINKVPLPVDKLAFLPLDNIIPFMDPLKLLKTLIGISV 60  
Db 1 MKLVTFLLVLTISLCSYSATAFINKVPLPVDKLAFLPLDNIIPFMDPLKLLKTLIGISV 60

QY 61 EHLVEGLRKCVELGPEASEAVKLLLEASHLV 93  
Db 61 EHLVEGLRKCVELGPEASEAVKLLLEASHLV 93

RESULT 6

ABU58521  
ID ABU58521 standard; protein; 93 AA.

AC ABU58521;

XX 15-APR-2003 (first entry)

XX Human PRO polypeptide #122.

XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy.

XX Homo sapiens.

XX US2003027272-A1.

XX 06-FEB-2003.

XX 21-JUN-2002; 2002US-00176492.

XX 18-SEP-1997; 97US-0059263P.

XX 18-SEP-1997; 97US-0059266P.

XX 17-OCT-1997; 97US-0062250P.

XX 21-OCT-1997; 97US-0063486P.

XX 24-OCT-1997; 97US-0063120P.

XX 24-OCT-1997; 97US-0063121P.

XX 28-OCT-1997; 97US-0063540P.

XX 28-OCT-1997; 97US-0063541P.

XX 28-OCT-1997; 97US-0063544P.

XX 28-OCT-1997; 97US-0063564P.

PR 21-NOV-1997; 97US-0066120P.  
PR 24-NOV-1997; 97US-0066466P.  
PR 24-NOV-1997; 97US-0066772P.  
PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 17-DEC-1997; 97US-0069870P.  
PR 18-DEC-1997; 97US-0068017P.  
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PR 16-SEP-1998;	98US-0101751P.		
PR 16-SEP-1998;	98US-01019330.		
PR 17-SEP-1998;	98US-0100683P.		
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ABUS8069

ABUS8069 standard; protein; 93 AA.

ABUS8069;

07-JUL-2003 (first entry)

Novel human secreted and transmembrane protein PRO1128.

Human; secreted and transmembrane protein: PRO; gene therapy; tumour necrosis factor-alpha release; TNF-alpha release; chondrocyte proliferation; chondrocyte differentiation; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.

Homo sapiens.

US2003032127-A1.

13-FEB-2003.

26-JUN-2002; 2002US-00183012.

18-SEP-1997; 97US-0059263P.

18-SEP-1997; 97US-0059266P.

17-OCT-1997; 97US-0062250P.

21-OCT-1997; 97US-0063486P.

24-OCT-1997; 97US-0063120P.

24-OCT-1997; 97US-0063121P.

28-OCT-1997; 97US-0063540P.

28-OCT-1997; 97US-0063541P.

28-OCT-1997; 97US-0063544P.

28-OCT-1997; 97US-0063564P.

29-OCT-1997; 97US-0063734P.

31-OCT-1997; 97US-0063870P.

31-OCT-1997; 97US-0064103P.

13-NOV-1997; 97US-0065311P.

21-NOV-1997; 97US-0066120P.



PR	23-SEP-1998;	98US-0101477P.	PR	18-DEC-1997;	97US-0068017P.
PR	24-SEP-1998;	98US-0101738P.	PR	10-MAR-1998;	98US-0077450P.
PR	24-SEP-1998;	98US-0101739P.	PR	11-MAR-1998;	98US-0077632P.
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PR	25-SEP-1998;	98US-0102330P.	PR	31-MAR-1998;	98US-0080107P.
PR	29-SEP-1998;	98US-0102331P.	PR	31-MAR-1998;	98US-0080194P.
PR	30-SEP-1998;	98US-0102487P.	PR	01-APR-1998;	98US-0080327P.
PR	30-SEP-1998;	98US-0102570P.	PR	01-APR-1998;	98US-0080333P.
PR	30-SEP-1998;	98US-0102571P.	PR	08-APR-1998;	98US-0081049P.
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PR	06-OCT-1998;	98US-0103258P.	PR	28-APR-1998;	98US-0083322P.
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Query Match 100.0%; Score 459; DB 6; Length 93;  
Best Local Similarity 100.0%; Pred. No. 5.6e-47;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLVTFILVITISLCSYSATAFINKVLPVDKLAFLPDLNLPMDPLKLLKTLGISV 60  
Db 1 MKLVTFILVITISLCSYSATAFINKVLPVDKLAFLPDLNLPMDPLKLLKTLGISV 60  
QY 61 EHLVEGLKCKVNELGPEASEAVKKLEALSHLV 93  
Db 61 EHLVEGLKCKVNELGPEASEAVKKLEALSHLV 93

RESULT 8  
ABU84384  
ID ABU84384 standard; protein; 93 AA.  
XX AC ABU84384;  
XX DT 02-AUG-2003 (first entry)  
XX DE Human secreted/transmembrane protein (PRO) #122.  
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;  
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing.  
XX OS Homo sapiens.  
XX PN US2003032112-A1.  
XX PD 13-FEB-2003.  
XX PF 21-JUN-2002; 2002US-00176756.  
XX PR 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059266P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
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Query Match 100.0%; Score 459; DB 6; Length 93;  
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DT 05-AUG-2003 (first entry)  
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XX KW Human; PRO; secreted protein; transmembrane protein;  
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
XX antiarthritic; vulnery; gene therapy.  
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XX XX  
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QY 61 EHLVEGLKRCVNELGPEASEAVKKLLLEALSHLV 93
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AC ABR5648;
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DT 05-AUG-2003 (first entry)
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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
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XX US2003036159-A1.
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PD 20-FEB-2003.
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KW chromosome mapping; gene mapping; cytostatic.
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RESULT 15
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DT 11-AUG-2003 (first entry)
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DE Human uteroglobin related protein 1.
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DE UGR21; human; mouse; promoter; uteroglobin related protein 1;
KW respiratory disorder; asthma.
XX
OS Homo sapiens.
XX
PN WO2J03000111-A2.
XX
PD 03-JAN-2003.
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PF 18-JUN-2002; 2002WO-US019456.
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PR 20-JUN-2001; 2001US-0299828P.
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PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kimura S, Niimi T;
XX
XX WPI; 2003-184004/18.
XX
PT New human UGRP1 nucleic acid, useful for diagnosing or predicting a
PT predisposition to develop a respiratory disorder or determining the
PT prognosis of a subject having or suspected of having a respiratory
PT disorder e.g., asthma.
XX
PS Disclosure; Page 79; 83pp; English.
XX
CC The present invention provides the human and murine uteroglobin related
CC protein 1 (UGRP1) promoters. The sequences can be used in the diagnosis
CC of and prediction of predisposition to respiratory disorders such as
CC asthma. The present sequence is a protein sequence shown in the
CC exemplification of the invention
XX
SQ Sequence 93 AA;

Query Match 100.0%; Score 459; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 5.6e-47;
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